REMARKS

Favorable reconsideration of the above-identified application in view of the amendments above and the remarks following is respectfully requested.

Claims 1, 4-8, 10-17 and 22-35 are pending in the application, of which Claims 5-8, 10-12, 16, 17 and 22-35 have been withdrawn. Claims 1, 4, and 13-15 have been rejected. Claims 1 and 13-15 have now been amended.

Specification

The Examiner states that the substitute specification filed August 19, 2008 is objected to under 35 U.S.C. 132(a) for introducing new matter into the disclosure of the invention.

The Examiner's objection is traversed.

Notwithstanding, please note that the specification has now been amended to provide the Affymetrix identification codename for the partial target sequence for which the Affymetrix probes were designed to hybridize with for all the Tables therein. Using these partial target code names it is possible to use Affymetrix software (available at the time of filing) to ascertain the target sequences for each gene. Applicant contends that provision of these code names enables anyone of ordinary skill in the art to carry out the presently claimed invention.

The specification teaches that the array used for Tables I-IV was U95Av2 - see page 38, line 16 of the amended specification and the array used for Table V was U133A - see page 38, line 17 of the amended specification. Although the code names of the partial target sequences were not disclosed in the original specification, these partial target sequences were available to the public at the time of filing. Accordingly, the addition of the code names for the partial target sequences does not add new matter to the specification.

In addition, the specification has also been amended to provide SEQ ID NOs. for the genes listed in Table II. The sequences provided are the most up-to date

sequences known at the time of filing of the application, and accordingly were the sequences used by Affymetrix to design their probes. Applicant contends that this approach also does not constitute addition of new matter.

The Examiner has also objected to the disclosure for referencing an incorrect Table number.

Please amend the paragraph on page 49 lines 12-18 as specified on Page 2:

The Examiner states that the amendment to the specification to insert the necessary language for the petition to accept color drawings is not compliant with 37 CFR 1.121.

Please add the paragraph specified on page 3 of this response to page 15, line 15 of the substitute specification such that it constitutes the first paragraph of the brief description of the drawings.

The Examiner has objected to the disclosure for containing embedded hyperlinks. Please amend the specification as indicated on Pages 3 and 4.

The Examiner states that it is improper to incorporate subject matter by reference to GenBank Accession numbers. Please note that the paragraph relating to incorporation of subject matter by reference to GenBank Accession numbers has been amended - see Page 11 of this response.

The Examiner has objected to the use of non-capitalized trademarks and their use without accompaniment of their generic terminology. Please amend the specification as indicated on Pages 6-11.

35 U.S.C. § 112, First Paragraph Rejections

The Examiner has rejected Claims 1, 4, and 13-15 under 35 U.S.C. § 112, first paragraph for failing to comply with the written description requirement.

The Examiner states that the sequence of the genes is essential matter for carrying out the invention. However, the Examiner states that addition of sequence ID numbers introduces new matter.

The Examiner's rejection is traversed.

Notwithstanding, Applicant has elected to cancel the matter that was incorporated into the specification in the response to the Office action of February 20, 2008. Instead, Applicant wishes to incorporate the sequences of the genes listed in Table II only. Please find enclosed a substitute specification which references each gene by a sequence ID number.

The sequences of all the genes provided correspond to the most up-to date sequence known at the time of filing.

As mentioned, Applicant has also amended the specification to incorporate the Affymetrix target ID for each gene. Applicant contends that addition of this matter now places the specification in condition for allowance.

The Examiner has rejected Claims 1, 4, and 13-15 under 35 U.S.C. § 112, first paragraph for failing to comply with the enablement requirement.

The Examiner states that the claims are too broad since they are not limited to the use of samples of peripheral blood mononuclear cells obtained from blood, nor does it limit the control samples, to ones which are age-matched or sex-matched. Further, the Examiner states that it would be unpredictable to compare the results obtained from a patient suffering from MS to the results obtained from a single healthy individual.

The Examiner concludes that such broad claims are not enabled.

The Examiner's rejections are traversed.

Notwithstanding, please note that the claims have now been limited to samples comprising peripheral blood mononuclear cells obtained from blood. Support for such a limitation can be found on Page 41, line 6.

Further, the control samples of Claim 1 have been limited to ones which are age and sex matched. Support for such an amendment can be found on Page 16, line 2 and Page 37, line 24 and Page 38, line 1.

Applicant wishes to point out that the specification teaches a group of genes whose expression may be used to diagnose whether a person has Multiple Sclerosis or not. These genes were identified by comparing a number of patient samples with a number of control samples. Selection of the genes was effected following complicated statistical analysis and care was taken to avoid counting genes which differ due to genetic heterogeneity. As such Applicant maintains that limitation of the control sample to an age and sex-matched sample is sufficient to increase the level of predictability and that one control sample is sufficient for performing the presently claimed method.

In view of the above amendments and remarks, it is respectfully submitted that claims 1, 4 and 13-15 are now in condition for allowance. An early Notice of Allowance is respectfully and earnestly solicited.

Respectfully submitted,

Martin D. Moynihan
Registration No. 40,338

Date: June 3, 2009

Enclosures:

Petition for Extension (Three Months)
Request for Continued Examination (RCE)
Replacement Sequence Listing on 3 CD-ROM's (1 CRF/ 2 Paper Format)
Annotated Marked-Up Specification
Substitute Specification

ANNOTATED MARKED-UP SPECIFICATION

PERIPHERAL BLOOD CELL MARKERS USEFUL FOR DIAGNOSING MULTIPLE SCLEROSIS AND METHODS AND KITS UTILIZING SAME

FIELD AND BACKGROUND OF THE INVENTION

The present invention relates generally to the field of diagnosis, treatment assessment and prognosis. More specifically, the present invention relates to peripheral blood cell expressed markers and kits and methods utilizing same for diagnosing, treating and assessing the state of multiple sclerosis (MS) in an individual. The present invention also provides cellular markers which are useful in distinguishing between different clinical courses of MS e.g.: probable, relapsing-remitting, secondary progressive or primary progressive as well as response to the therapy.

Multiple sclerosis is an autoimmune neurodegenerative disease, which is marked by inflammation within the central nervous system with lymphocyte attack against myelin produced by oligodendrocytes, plaque formation and demyelization with destruction of the myelin sheath of axons in the brain and spinal cord, leading to significant neurological disability over time. The disease frequently occurs in young adults between 20-40 years of age, is more prevalent in females than males (2:1), and has a characteristic geographical distribution – estimated prevalence in USA 120/100,000, (250,000 to 350,000 cases).

The annual cost of MS in USA was estimated about $34,000 per person, $2.2 million total lifetime cost per case or $6.8 billion yearly, in a conservative estimate of a national annual cost (Anderson DW, 1992; Whetten-Goldstain K., 1998).

Clinical Diagnosis and Evaluation of Stages of MS

Typically, at onset an otherwise healthy person presents with the acute or sub acute onset of neurological symptomatology (attack) manifested by unilateral loss of vision, vertigo, ataxia, dyscoordination, gait difficulties, sensory impairment characterized by paresthesia, dysesthesia, sensory loss,

urinary disturbances until incontinence, diplopia, dysarthria or various degrees of motor weakness until paralysis. The symptoms are usually painless, remain for several days to a few weeks, and then partially or completely resolve. After a period of remission, a second attack will occur. During this period after the first attack, the patient is defined to suffer from probable MS. Probable MS patients may remain undiagnosed for years. When the second attack occurs the diagnosis of clinically definite MS (CDMS) is made (Poser criteria 1983; C.M. Poser et al., Ann. Neurol. 1983;13, 227).

The clinical disease courses of MS are relapsing-remitting, primary or secondary progressive (Abramsky, 1997; Russell, 1998).

The relapsing-remitting course of MS (85% of patients) is characterized by acute attacks or relapses during which new neurological symptoms and signs appear, or worsen. Relapse develops within a period of several days, lasts for 6-8 weeks, than gradually resolves. During the acute relapse scattered inflammatory and demyelinating central nervous system (CNS) lesions produce varying combinations of motor, sensory, coordination, visual, and cognitive impairments, as well as symptoms of fatigue and urinary tract dysfunction. The outcome of a relapse is unpredictable in terms of neurological sequel but it is well established that with additional relapses, the probability of complete clinical remission decreases and neurological disability and handicap may develop. On average, about 60% of patients remain fully functional 10 years after the primary attack, and 25 to 30% remain fully functional 30 years after onset. Statistically, the disease does not greatly decrease life expectancy (mean decrease 12 years), although some patients become severely disabled and die from recurrent infections and complications.

Primary progressive MS (10% of patients) is characterized by slow, progressive neurological dysfunction usually in the form of a gradual myelopathy causing spasticity and ataxia. Treatment regimen varies greatly with different clinical course and severity of the disease.

The diagnosis of MS is still defined primary by clinical terms and relies on a combination of history, neurological examination and ancillary laboratory and neuro-imaging studies.

Laboratory tests for MS include: 1) CSF evaluation of IgG synthesis, oligoclonal bands; 2) MRI of the brain and spinal cord and; 3) exclusion of other autoimmune diseases by blood tests [e.g.,; serum B12 level; HTLV 1 or HIV 1 titers; sedimentation rate or C-reactive protein; RA latex (Rheumatoid arthritis); ANA, anti-DNA antibodies (systemic lupus erythematosus)]. However, accurate diagnosis and prognosis in the "probable" stage, and early relapsing-remitting stages remains problematic. For example, it has been shown that positive MRI findings in the first demyelinating attack only provide a 50% successful prediction of development of clinically definite MS within 2-3 years (CHAMPS Study Group, Neurology 2002;59:998-1005). Likewise, Villar et al (Neurology 2002;59:877-83) found that detection of oligoclonal IgM bands with early symptoms were only partially predictive of development of clinically definite MS.

Other laboratory tests may provide some additional support for the diagnosis, but evidence of lesions disseminated in time and space remains a cardinal element of the diagnosis (Poser CM., 2001). In absence of definitive laboratory tests and pathognomonic clinical features, MS remains ultimately a diagnosis of exclusion.

Diseases that may be confused with MS are: 1) Acute disseminated encephalomyelitis (follows infections or vaccination mainly in children, fever, headaches, and meningitis common), 2) Lyme disease (antibodies to Borrelia species antigens in serum and CSF), 3) HIV associated myelopathy (HIV antibodies present), 4) HTLVI myelopathy (HTLVI antibodies present in serum/CSF), 5) Neurosyphilis (syphilis antibodies present in serum and/or CSF, 6) Progressive multifocal leukoencephalopathy (biopsy of lesions demonstrates virus by electron microscopy), 7) Systemic lupus erythematosus (CNS

manifestations of lupus, antinuclear antibodies, anti-dsDNA), 8) Polyarteritis nodosa (systemic signs, micro-aneurysms demonstrated by angiographies, vasculitis demonstrated in biopsy of involved areas), 9) Sjogren's syndrome (dry eyes and mouth, antiRo and antiLa antibodies), 10) Behcet's disease (Oral/genital ulcers, antibodies to oral mucosa), 11) Sarcoidosis (CNS signs, increased protein in CSF, biopsy shows granuloma, 12) Paraneoplastic syndromes (older age group, antiYo antibodies), 13) Subacute combined degeneration of cord (peripheral neuropathy, vitamin B12 levels), 14) Sub acute myeloopticoneuropathy (adverse reaction to chlorhydroxyquinoline, mainly in Japanese), 15) Hereditary spastic paraparesis/ primary lateral sclerosis (normal CSF, MRI and visual evoked potential studies), 16) Adrenomyeloneuropathy (adrenal dysfunction, neuropathy, increased plasma very long-chain fatty acids), 16) Spinocerebellar syndromes (familial, pes cavus scoliosis, abnormal reflexes, normal CSF IgG), 17) Miscellaneous – strokes, tumors, arteriovenous malformations, arachnoid cysts, Arnold-Chiari malformations, and cervical spondylosis all may lead to diagnostic dilemmas on occasion. Thus, detailed history and neurological examination must be complemented by specific laboratory tests for the correct diagnosis of MS. Clearly there is a long felt need for more powerful diagnostic tools for prediction and staging of MS.

Etiology of MS

The etiology of MS is unknown. It is suggested that a combination of genetic background and environmental factors and immune response are involved in the disease. A certain incidence of familial occurrence has been observed, with the concordance rate among monozygotic twins being 30%, a 10-fold increase over that in dizygotic twins or first-degree relatives (Steinman, 1966; Dyment et al Mol. Gen 1997;6:1693-98). In addition, recent research indicates that the tissue damage in MS occurs as the result of pathological autoimmune responses to several myelin antigens following exposure to an as yet undefined environmental causal agent.

However, although some environmental factors have been statistically associated with the disease, none have provided correlations of any predictive value. Environmental factors seem to trigger MS in subjects who are already genetically susceptible to the illness. Most probably no one dominant gene determines genetic susceptibility, but rather many genes, each with different influence, are involved. Indeed, the initial pathogenic process could be caused by one group of genes, while others groups could be responsible for the development and progression of the disease (Oksenberg, 2001; Compston, 1997).

Microarray Analysis and MS

Microarray technology is based on hybridization of mRNA to high-density array of immobilized target sequences. Each sequence corresponds to a specific gene(s) of interest. The labeled pool of sample mRNA is subsequently hybridized to the array (chip). Application of this technology provides the capability of monitoring thousands of various genes simultaneously. Today commercial available DNA microarrays (Affymetrix, Santa Clara CA, USA) contain elements representing 10,000, 20,000 or more genes that have been characterized in terms of function or disease association. The preparation and use of microarrays for diagnostics, research and drug development is disclosed in, inter alia, US Pat. Nos. 6,324,497 and 6,468,476 to Friend et al and 6,410,229 to Lockhart et al; and Intnl Pat. Application WO 0053625C2 and A2.

Several application of microarrays in human disease have been reported, for example the identification (marker) genes involved in ovarian carcinogenesis (Ono K., 2000); classification of genes expression profiling of cutaneous malignant melanoma (Bitter M., 2000); and expression profile of Tangl-Rearing CA1 neurons in Alzheimer's disease (Stephen, 2000). Alizaden (2000) characterized gene expression in diffuse large B cell lymphoma, where two distinct gene expression patterns, characterized by different molecular forms of B cells lymphoma, were identified. In addition, microarray

technology has also been applied to diagnosis and monitoring of such diverse diseases as cancer (US Pat. No. 6,511,849 to Freuhauf et al), psoriasis (Intnl Pat. Application WO 20020027538 to Trepicchio et al), T-helper cell related diseases (Trepicchio et al , Intnl Pat Application WO 20020039734), Epstein-Barr disease (U.S. Pat. Nos. 6,506,553 and 6,468,476 to Smith and Parks), rheumatoid arthritis (Intnl Pat Application WO 0248310A2 to Trepicchio et al) and Reward Deficiency Syndrome, all of which are incorporated herein by reference.

In a recent review (Greenberg SA., 2001) the author discussed the potential application of DNA microarray technology for understanding neurological disorders. Using cDNA microarrays technology, brain tissue from pathology lesions and normal white matter of single MS patient were analyzed (Whitney LW.,1999). Blood genomic fingerprints were demonstrated after experimental strokes, seizures, hypoglycemia and hypoxia of rats (Yang Tang, 2001). Similarly, microarray analysis of gene expression in brainstem and spinal cord tissues from the animal models of MS (experimental autoimmune encephalomyelitis, EAE) has identified a number of differentially expressed genes from active-acute versus silent lesions (Lock C. et al Nat Med 2002;8,500-504), and also suggested a role for the proinflammatory cytokine osteopontin in the development of EAE in mice (Chabas D et al Science 2001;294:1731-34).

In another recent study, Ramanathan M et al (J of Immunology 2001;116:213-19) used cDNA microarray technology to identify abnormal gene expression patterns in PBMC of relapsing-remitting MS patients. The study compared PBMC gene expression in 15 patients during remission (only) with that of 15 healthy controls, using a GeneFilters GF211 array (Research Genetics, Huntsville AL, USA) having approximately 5200 human gene sequences. Groups of marker genes correlated with MS were disclosed, but the range of differences (fold changes) between level of gene expression in MS and

control groups was only 13 to 35 % for unregulated and from 11 to 43% for down regulated genes. Such small differences are probably due to the limited sensitivity of the technology employed in using GeneFilters arrays, and may not have any clinical or diagnostically mining significance. More significantly, the population of MS patients was limited, including only patients during clinical remission, who had not received any immunosupressive treatment for at least 3 months. Thus, the markers described do not provide a profile of expression patterns useful for diagnosing clinically defined MS in patients having probable MS, or for determining stages of the disease.

Trepicchio et al. (Intnl Pat. Application No. WO 02/079218 A1) also describe the use of microarray technology in determining characteristic gene expression in an animal model of MS (murine EAE) and in tissue samples from MS patients. The human samples were PBMC or brainstem tissue, collected from 60 patients manifesting a wide variety of symptoms, at different stages of MS including relapsing-remitting, primary and secondary progressive, and acute exacerbation. RNA probes prepared from these samples were hybridized to a human chip array containing approximately 14,000 gene sequences (MicroArray, Affymetrix, cat no. 510448, Santa Clara CA), and expression profiles compared with those of healthy controls. Determination of the panel of "MS-related" markers was based merely on fold change of greater than 2 fold (up- or downregulated), with a confidence level of $p<0.01$. No more stringent statistical criteria were applied. A "panel" of 300 differentially regulated genes was thus described in the PBMC samples, and another 100 in the brain lesion tissue. However, no classification of expression profiles characteristic to specific stages of the disease was provided, and the "class predictor model", as described, using "neighborhood analysis", was applied for attempted prediction of "MS-afflicted" or "non-diseased" samples only. Thus, the panel of markers described is not applicable to the diagnosis of stage of MS, in general, is

unsuited for the prediction of clinically definite MS or probable MS patients, and is clearly non-predictive in monitoring response to treatment.

There is thus a widely recognized need for, and it would be highly advantageous to have gene expression profiles useful in distinguishing between different forms of MS e.g.: probable, relapsing-remitting, primary or secondary as well as response to the therapy, devoid of the above limitations.

SUMMARY OF THE INVENTION

According to one aspect of the present invention there is provided a method of diagnosing a subject with multiple sclerosis, the method comprising determining a level of expression of at least one gene selected from the group consisting of the genes listed in Tables I-V in a sample obtained from the subject, wherein a substantial difference between the level of expression of the gene in the sample obtained from the subject and a normal expression level of the gene is an indication that the subject is afflicted with multiple sclerosis.

According to further features in preferred embodiments of the invention described below a method of monitoring a state of multiple sclerosis in a subject, the method comprising monitoring a level of expression of at least one gene selected from the group consisting of the genes listed in Tables I-V over a predetermined time period, wherein substantial difference between the levels of expression of the at least one gene over the predetermined time period indicates a change in a state of the multiple sclerosis in the subject.

According to further features in preferred embodiments of the invention described below monitoring the level of expression of at least one gene over the predetermined time period is effected by periodically obtaining a sample from the individual and determining the level of expression of the at least one gene in the sample.

According to still further features in the described preferred embodiments the at least one gene comprises at least 10, at least 50, at least 100, at least 250, at least 500, at least 750, at least 1000 or at least 1200 genes

each independently selected from the group consisting of the genes listed in Tables I-V.

According to another aspect of the present invention there is provided a method of diagnosing a subject with multiple sclerosis, the method comprising the step of determining a level of expression of each of the genes listed in Tables I-V in a sample obtained from the subject, wherein a substantial difference between expression levels of the genes in the sample obtained from the subject and normal expression levels of the genes is an indication that the subject is afflicted with multiple sclerosis.

According to further features in preferred embodiments of the invention described below the normal expression level of the at least one gene or genes is determined by measuring the level of expression of the gene or genes in at least one control sample obtained from at least one healthy individual.

According to still further features in the described preferred embodiments the sample includes peripheral blood mononuclear cells.

According to yet further features in the described preferred embodiments the substantial difference is a difference statistically significant at a confidence level of $p= 0.05$ as determined by at least one test selected from the group consisting of a t-test, a TNoM and an INFO score.

According to further features in preferred embodiments of the invention described below the level of expression of the at least one gene or genes is determined by quantifying a level of a protein product thereof in the sample.

According to still further features in the described preferred embodiments quantifying a level of the protein is effected using a reagent which specifically binds with the protein.

According to yet further features in preferred embodiments of the invention described below the reagent comprises an antibody or fragments thereof.

According to further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table I.

According to still further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table II.

According to yet further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table III.

According to further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table IV.

According to still further features in the described preferred embodiments at least one gene or genes are selected from the genes listed in Table V.

According to yet further features in preferred embodiments of the invention described below the level of expression of the at least one gene or genes in the sample is determined by detecting the presence in the sample of a transcribed polynucleotide or portion thereof. The transcribed polynucleotide can be mRNA.

According to further features in preferred embodiments of the invention described below the transcribed polynucleotide or portion thereof is detected via a labeled probe which specifically hybridizes with the transcribed polynucleotide or portion thereof.

According to still further features in the described preferred embodiments the sample from a subject is T cells, the at least one gene or genes are selected from the genes listed in Table IV and the normal expression of the gene or genes is T-cell expression.

According to an additional aspect of the present invention there is provided a method of assessing the efficacy of a treatment regimen on multiple sclerosis in a subject, the method comprising determining a level of expression of at least one gene or genes selected from the group consisting of the genes listed in Tables I-V in samples obtained from the subject prior to, and following exposure to the treatment regimen, wherein a substantial difference in the expression level of at least one gene or genes between the samples is an indication that the treatment regimen is efficacious in treating multiple sclerosis in the subject.

According to further features in preferred embodiments of the invention described below the treatment regimen is administering at least one test compound for inhibiting multiple sclerosis.

According to still further features in the described preferred embodiments the treatment regimen is an environmental condition.

According to yet further features in the described preferred embodiments the substantial difference is a difference statistically significant at a confidence level of $p= 0.05$ as determined by at least one test selected from the group consisting of a t-test, a TNoM and an INFO score.

According to further features in preferred embodiments of the invention described below the level of expression of the at least one gene or genes is determined by quantifying a level of a protein product thereof in the sample.

According to still further features in the described preferred embodiments quantifying a level of the protein is effected using a reagent which specifically binds with the protein.

According to yet further features in preferred embodiments of the invention described below the reagent comprises an antibody or fragments thereof.

According to further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table I.

According to still further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table II.

According to yet further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table III.

According to further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table IV.

According to still further features in the described preferred embodiments at least one gene or genes are selected from the genes listed in Table V.

According to yet further features in preferred embodiments of the invention described below the level of expression of the at least one gene or genes in the sample is determined by detecting the presence in the sample of a transcribed polynucleotide or portion thereof. The transcribed polynucleotide can be mRNA.

According to further features in preferred embodiments of the invention described below the transcribed polynucleotide or portion thereof is detected via a labeled probe which specifically hybridizes with the transcribed polynucleotide or portion thereof.

According to still further features in the described preferred embodiments the sample from a subject is T cells, the at least one gene or genes are selected from the genes listed in Table IV and the normal expression of the gene or genes is T-cell expression.

According to still further features in the described preferred embodiments the at least one gene comprises at least 10, at least 50, at least 100, at least 250, at least 500, at least 750, at least 1000 or at least 1200 genes each independently selected from the group consisting of the genes listed in Tables I-V.

According to another aspect of the present invention there is provided a kit for diagnosing multiple sclerosis in a subject, the kit comprising components suitable for determining expression levels of at least one gene selected from the group of genes listed in Tables I-V.

According to further features in the described preferred embodiments the reagents include at least one polynucleotide sequence selected capable of specifically hybridizing with an transcription product of the at least one gene and reagents for detecting and optionally quantifying a complex formed from the at least one polynucleotide sequence and said transcription product.

According to still further features in the described preferred embodiments the reagents include at least one antibody selected capable of specifically binding a polypeptide product of the at least one gene and reagents for detecting and optionally quantifying a complex formed from the at least one antibody and the polypeptide product.

According to further features in preferred embodiments of the invention described below the at least one gene is selected from the genes listed in Table I.

According to still further features in preferred embodiments of the invention described below the at least one gene is selected from the genes listed in Table II.

According to yet further features in preferred embodiments of the invention described below the at least one gene is selected from the genes listed in Table III.

According to further features in preferred embodiments of the invention described below the at least one gene is selected from the genes listed in Table IV.

According to still further features in the described preferred embodiments at least one gene is selected from the genes listed in Table V.

According to further features in preferred embodiments of the invention described below the kit further comprises packaging material identifying the kit as useful from diagnosing MS.

According to another aspect of the present invention there is provided a polynucleotide array comprising at least 10 and no more than 1500 polynucleotide sequences, wherein each of the sequences is selected capable of hybridizing with a transcription product of a polynucleotide sequence of a gene selected from the group of genes listed in Tables I-V.

According to further features in preferred embodiments of the invention described below the array is selected having polynucleotide sequences capable of diagnosing subjects suspected of suffering from multiple sclerosis. The subjects may also be suspected of suffering from probable multiple sclerosis, primary progressive multiple sclerosis, secondary progressive multiple sclerosis, and/or relapsing/remitting multiple sclerosis.

According to further features in preferred embodiments of the invention described below the gene is selected from the genes listed in Table I, II, III, IV and/or IV.

According to yet another aspect of the present invention there is provided an array comprising at least 10 and no more than 1500 antibodies or antibody fragments each capable of specifically binding a protein product of a gene selected from the group of genes listed in Tables I-V.

According to further features in preferred embodiments of the invention described below the array is selected having antibodies or antibody fragments capable of diagnosing subjects suspected of suffering from multiple sclerosis.

The subjects may also be suspected of suffering from probable multiple sclerosis, primary progressive multiple sclerosis, secondary progressive multiple sclerosis, and/or relapsing/remitting multiple sclerosis.

According to further features in preferred embodiments of the invention described below the gene is selected from the genes listed in Table I, II, III, IV and/or IV.

Implementation of the method and system of the present invention involves performing or completing selected tasks or steps manually, automatically, or a combination thereof. Moreover, according to actual instrumentation and equipment of preferred embodiments of the method and system of the present invention, several selected steps could be implemented by hardware or by software on any operating system of any firmware or a combination thereof.

BRIEF DESCRIPTION OF THE DRAWINGS

The invention is herein described, by way of example only, with reference to the accompanying drawings. With specific reference now to the drawings in detail, it is stressed that the particulars shown are by way of example and for purposes of illustrative discussion of the preferred embodiments of the present invention only, and are presented in the cause of providing what is believed to be the most useful and readily understood description of the principles and conceptual aspects of the invention. In this regard, no attempt is made to show structural details of the invention in more detail than is necessary for a fundamental understanding of the invention, the description taken with the drawings making apparent to those skilled in the art how the several forms of the invention may be embodied in practice.

In the drawings:

FIGs. 1A-B are graphic representations of the differences in PMBC gene expression between MS patients and healthy subjects. RNA from Peripheral

Blood Mononuclear Cells (PMBC) of 26 patients diagnosed with MS, and 18 healthy, age-matched controls was purified, labeled hybridized to a Genechip array (U95Av2, Affymetrix Inc. Santa Clara CA, USA), scanned and analyzed according to manufacturer's recommendations. The data were normalized and fold ratios calculated for each gene of the MS samples against the geometric mean of the controls. Figure 1A shows the number of MS specific genes detected having increased expression (fold change greater than 1.5) analyzed by t-test (red line), TNoM (green line) and INFO (blue line), compared with random occurrence (black line), at confidence levels (False Discovery Rates, FDR) of 90% (p= 0.10) to 100% (p= 0). Note the high level of significant MS-related gene expression at 95% FDR and above (arrows) (1249 distinguished genes). Figure 1B is an infogram of the 1249 genes most significantly ($p<0.05$ on all three tests) distinguishing MS patients (MS) from (control) healthy controls, determined as above. Each spot represents expression of a specific gene; color intensity of overexpressed (green) and under-expressed (red) genes indicates fold increase as compared to controls. Gray color indicates genes showing no difference in expression between MS and controls.

FIGs. 2A-B are graphic representations of the differences in PMBC gene expression between MS patients during acute relapse, and MS patients in remission. RNA from PMBC of 12 relapsed, and 14 clinically in remission patients was purified, labeled, hybridized and analyzed as described for Figures 1A-B hereinabove. Figure 2A shows the number of acute relapse-specific genes detected having increased expression in relapse, as analyzed by t-test (red line), TNoM (green line) and INFO (blue line), compared with random occurrence (black line), at confidence levels (False Discovery Rates, FDR) of 90% (p= 0.10) to 100% (p= 0). 735 genes were detected having significant relapsing-related gene expression at 95% FDR and above. Figure 2B is an infogram analysis of the 735 genes most significantly ($p<0.05$ on all three tests) distinguishing acute relapsing MS patients (Relapse) from MS patients in

remission (Remission). Note the different profiles of gene expression in patients undergoing treatment (Relapse + and Remission +) compared with untreated patients (Relapse- and Remission -).

FIG. 3 is a pie chart diagram showing the breakdown, by functional character, of specific genes displaying up- or down-regulation in MS-derived MOG-reactive T-cell lines, as compared to normal-derived MOG-reactive T-cell lines. Significant MOG reactive MS-related genes are defined as genes with TNoM=0 and p=0.057 as compared to normal MOG-reactive T-cells.

FIG. 4 is a graphic representation of the differences in gene expression between MOG-stimulated T-cell lines from MS patients and healthy controls. RNA from MOG-stimulated T-cells of 4 MS patients and 3 matched controls was purified, labeled, hybridized and analyzed as described for Figures 1A-B hereinabove. Panel A shows a cluster analysis of 150 differentially expressed genes analyzed as described hereinabove (TNoM=0, $p<0.05$) distinguishing T-cells of MS (MS) patients from controls (Controls). Panel B shows a cluster analysis of the 43 most informative genes (TNoM=0, $p<0.05$, and fold change> 1.5). Each row represents a gene, and each column represents a T-cell line form a different subject. Yellow color indicates genes with an increased expression relative to controls are yellow, and blue color indicates genes with relative decreased expression.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention is of methods and kits for diagnosing multiple sclerosis in subjects, using novel gene expression profiles derived from peripheral blood cells. Specifically, the present invention can be used to diagnose MS in early stages of the disease, to determine clinical stage and predict the course of the disease in patients with a unclear diagnoses, to provide definition and prognostic information in patients with probable MS, to assess

and monitor MS therapies and to screen new and established drugs and treatments for MS.

The principles and operation of the present invention may be better understood with reference to the drawings and accompanying descriptions.

Before explaining at least one embodiment of the invention in detail, it is to be understood that the invention is not limited in its application to the details of construction and the arrangement of the components set forth in the following description or illustrated in the Examples and drawings. The invention is capable of other embodiments or of being practiced or carried out in various ways. Also, it is to be understood that the phraseology and terminology employed herein is for the purpose of description and should not be regarded as limiting.

The present invention provides previously unavailable accuracy in predicting and staging MS, by identifying genes and groups of genes specifically over- and under-expressed in PBMC of patients at various stages of their disease.

As is further described in the Examples section which follows, the present inventors have conducted a broad scale analysis of PMBC expressed genes using hybridization of biotin-labeled PBMC mRNA to more than 12,000 human gene sequences provided on DNA chips. By utilizing specialized statistical analysis approaches, the present inventors identified in the microarray data the most highly informative expression profiles.

As mentioned hereinabove, multiple sclerosis is a chronic, multi-factorial neurodegenerative disease of unknown etiology, the diagnosis and classification of which remains largely clinical in nature. Identification of the stages and progression of the disease, particularly definition of the probable MS stage, is crucial to determination of optimal treatment regimen and development of effective therapies. However, the complexities of autoimmune interactions, and the variability of MS in different individuals have made diagnosis and

subsequent prognosis using traditional methods inexact and challenging. Methods for more accurate diagnosis of MS are greatly needed.

The profiles of MS-related genetic markers listed in Table I represent genes exhibiting differential expression in PBMCs from a large sample of MS patients, compared to that of age-matched healthy controls. Abundance of specific gene transcripts, represented by the intensity of label hybridizing to individual sequence loci of the MicroArray (Affymetrix Inc, Santa Clara CA), was recorded and quantified according to the manufacturers recommended protocols (such as GeneChip 3.0 software from Affymetrix). However, rather than composing the profile of differentially expressed genes based on probabilities using simple distribution of mean intensities, as has been reported by Ramanathan et al (J Immunol 2001;116:213-219), informative genes were selected based on the degree to which they were predictive of classification of the sample as "diseased" or "not diseased". By applying the rigorous three-pronged statistical analysis described in detail hereinbelow, 1249 genes most informative in distinguishing between diseased and otherwise not diseased patients were identified (see Table I). By applying an even more restrictive analysis of the data in Table I (see Table II, Bonfferoni analysis), a subset of the 300 highest scoring genes was identified. These MS marker genes comprise both over-expressed and downregulated genes, and represent of a diverse group of functional gene categories. Additional analysis of the markers uncovered herein also led to the identification of another restricted marker set which can be accurately utilized to diagnose probable MS patients. As is further described hereinbelow, the identification of such a marker set represents a significant breakthrough since it enables to treat individuals at a much earlier stage of MS then previously possible.

Thus, according to one aspect of the present invention there is provided a method of diagnosing a subject with multiple sclerosis by determining a level of expression of at least one gene of the genes listed in Tables I-V in a sample

obtained from the subject, wherein a substantial difference between the level of expression of the gene in the sample obtained from the subject and a normal expression level of the gene is an indication that the subject is afflicted with multiple sclerosis.

Normal expression levels of a marker or markers are obtained from isolated or cultured PMBCs (e.g., T-cell cultures), or samples obtained from individuals not affected with MS. A substantial difference is preferably of a magnitude that is statistically significant (see the Examples section for more detail). In particularly preferred embodiments, the marker is increased or decreased relative to control samples by at least 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, or 10-fold or more. Similarly, one skilled in the art will be well aware of the fact that a preferred detection methodology is one in which the resulting detection values are above the minimum detection limit of the methodology utilized.

As is further described in the Examples section which follows, the marker listed in Tables I-V were identified in peripheral blood cells. As such, the sample obtained from the individual is preferably a peripheral blood sample or any sample which includes blood cells such as T-cells. In a preferred embodiment, the sample is blood, thymus, spleen, lymph, pus, or bone marrow. However, it will be apparent to one skilled in the art that PMBCs may be present as an infiltrate in many other tissues, and that such tissues may also serve as samples in which the presence, activity, and/or quantity of the markers of the invention may be assessed. The tissue samples containing one or more of the markers themselves may be useful in the methods of the invention, and one skilled in the art will be well aware of methods by which such samples may be conveniently obtained, stored, preserved and processed. For further description relating to collection and processing of blood samples please see the Examples section which follows.

As is detailed in the Examples section below, analysis of PBMC genes differentially expressed in MS, according to the methods described herein,

revealed groups of genes of specific interest in MS. Genes that are most significantly over expressed, or downregulated in MS can indicate members of pathways important to disease development or pathology. Strongly overexpressed genes, according to Tables I and II, include **SLAM** (signaling lymphocyte activation molecule, GenBank Accession No. U33017), **LEF1** (lymphoid enhancer-binding factor 1, GenBank Accession No. AL099409), **LRP5** (low density lipoprotein receptor-related protein 5, GenBank Accession No. AF077820), **LILRB** (leukocyte immunoglobulin-like receptor, GenBank Accession No. AF004230), **LY75** (lymphocyte antigen 75, GenBank Accession No. AF011333), **CDW52** (GenBank Accession No. N90866), **PIP5K1-gamma** (Phosphatidylinositol-4-phosphate 5-kinase, type 1, gamma, GenBank Accession No. AB011161), **MAP4** (Microtubule-associated protein 4, GenBank Accession No. M64571), **CTSK** (Cathepsin K, GenBank Accession No. X82153) and **CTSB** (Cathepsin B, GenBank Accession No. L22507). Strongly down-regulated genes include **IL1B** (Interleukin 1 beta, GenBank Accession No. M15330), **TRAF6** (GenBank Accession No. U78798), **SCYA20** (GenBank Accession No. U64197), **IL1R** (type1 receptor, GenBank Accession No. M27492), **IL1RAP** (receptor accessory protein, GenBank Accession No. AB006537) and **IL1RN** (receptor antagonist, GenBank Accession No. X52015), **TGFB1** (Transforming growth Factor beta 1, GenBank Accession No. X05839), **SKI** (v-ski sarcoma viral oncogene homologue, GenBank Accession No. X15218), **VEGF** (Vascular endothelial growth factor, GenBank Accession No. M63978), **IGFBP4** (Insulin-like growth factor binding protein 4, GenBank Accession No. U20982), **EREG** (epiregulin, GenBank Accession No. NM_001432.1), and **NR4A1, NR4A2, NR4A3** (nuclear receptor family genes, GenBank Accession Nos. NM_002135.1, X75918 and U12767, respectively).

Functional groups of genes strongly represented in the profile of most significantly differentially regulated genes in MS include, inter alia, apoptosis-

related genes, T-cell activation and expansion related genes, cell proliferation related genes and epidermal growth factor genes. Many of the marker genes identified are associated with other MS- related genes, according to Tables I-V.

It will be appreciated that although a single marker can be used for diagnosis, diagnostic accuracy typically increases with an increase in the number of markers utilized.

As such, the diagnostic method of the present invention preferably utilizes a marker set that can range anywhere from 2 genes to 1200 genes. For example, the present method can utilize at least 10, at least 50, at least 100, at least 250, at least 500, at least 750, at least 1000 or at least 1200 genes each independently selected from the group consisting of the genes listed in Tables I-V. Most preferably the markers utilized are selected from the sequences listed in Table II.

The markers sets utilized can be selected according to a statistical significance or fold change thereof (provided for each marker in Tables I-V), a higher significance and higher fold change indicating higher probability of marker accuracy. For example, a selected marker set can encompass markers displaying a high statistical significance (low P-value), preferably a P-value lower than 5.0E-02, more preferably lower than 5.0E-04, most preferably, lower than 5.0E-06. Alternatively, markers can be selected according to shared features of the marker gene. For example, gene markers of similar cellular function (e.g., genes of a signaling pathway such as apoptosis) or markers displaying similar activity (e.g., enzymes of the same enzyme family) can be grouped into specific marker sets.

Each marker set may be considered individually, although it is within the scope of the invention to provide combinations of two or more marker sets for use in the methods and compositions of the invention to increase the confidence of the analysis.

As used herein, the terms "polynucleotide" and "oligonucleotide" are used interchangeably, and include polymeric forms of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Polynucleotides may have any three-dimensional structure, and may perform any function, known or unknown. The following are non-limiting examples of polynucleotides: a gene or gene fragment, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component. The term also includes both double- and single-stranded molecules. Unless otherwise specified or required, any embodiment of this invention that is a polynucleotide encompasses both the double-stranded form and each of two complementary single-stranded forms known or predicted to make up the double-stranded form.

As used herein, a "gene" includes a polynucleotide containing at least one open reading frame that is capable of encoding a particular polypeptide or protein after being transcribed and translated. Any of the polynucleotide sequences described herein may be used to identify larger fragments or full-length coding sequences of the gene with which they are associated. Methods of isolating larger fragment sequences are known to those of skill in the art, some of which are described herein. A "gene product" includes an amino acid (e.g., peptide or polypeptide) generated when a gene is transcribed and translated.

As used herein, a "probe" is defined as an oligonucleotide that is provided as a reagent to detect a target present in a sample of interest by hybridizing with the target. Usually, a probe will comprise a label or a means by which a label can be attached, either before or subsequent to the hybridization reaction. Suitable labels include, but are not limited to radioisotopes, fluorochromes, chemiluminescent compounds, dyes, and proteins, including enzymes.

As used herein, "expression" includes the process by which polynucleotides are transcribed into mRNA and translated into peptides, polypeptides, or proteins. "Differentially expressed", as applied to a gene, includes the differential production of mRNA transcribed from a gene or a protein product encoded by the gene. A differentially expressed gene may be overexpressed or underexpressed as compared to the expression level of a normal or control cell. In one aspect, it includes a differential that is 2.5 times, preferably 5 times or preferably 10 times higher or lower than the expression level detected in a control sample. The term "differentially expressed" also includes nucleotide sequences in a cell or tissue which are expressed where silent in a control cell or not expressed where expressed in a control cell.

As used herein, the term "polypeptide" is defined as a compound of two or more subunit amino acids, amino acid analogs, or peptidomimetics. The subunits may be linked by peptide bonds. In another embodiment, the subunit may be linked by other bonds, e.g., ester, ether, etc. As used herein the term "amino acid" includes either natural and/or unnatural or synthetic amino acids, including glycine and both the D or L optical isomers, and amino acid analogs and peptidomimetics. A peptide of three or more amino acids is commonly referred to as an oligopeptide. Peptide chains of greater than three or more amino acids are referred to as a polypeptide or a protein.

As used herein, the term "marker" is defined as a polynucleotide or polypeptide molecule which is present or absent, or increased or decreased in

quantity or activity in subjects afflicted with multiple sclerosis, or in cells involved in multiple sclerosis. The relative change in quantity or activity of the marker is correlated with the incidence or risk of incidence of multiple sclerosis or progression from one stage of the disease to another.

Although all of the markers listed in Tables I-V can be used in diagnosis of MS, an additional object of the present invention was to identify those markers which can be utilized to diagnose specific clinical forms and/or stages of MS.

Accurate clinical tools for specific diagnosis of disease stages in MS are presently unavailable.

As a result of comprehensive studies conducted in efforts to evaluate specific gene expression in relation to clinical disease phases, the present invention provides, for the first time, specific markers sets which can be utilized in accurate diagnosis of specific forms and stages of MS

As is illustrated in Example II of the Examples section which follows, the present invention provides marker sets which can be accurately utilized to diagnose acute relapse, remission and probable stages of MS (Tables III-V).

Of particular importance is the marker set provided in Table V. As is described in the Examples section which follows, the present inventors also uncovered cellular markers which distinct between disease-related and non-disease related T-cell myelin reactivity. Although MS appears to be caused by autoimmune T-cells activated against myelin self-antigens, myelin-reactive T-cells have been demonstrated in healthy subjects as well. Thus, distinction between disease-related and non-disease related T-cell myelin reactivity is of great clinical and investigational importance.

Cellular markers which distinct between disease-related and non-disease related T-cell myelin reactivity include down-regulating apoptosis associated genes, up regulating anti-apoptotic genes and genes responsible for increased expansion capability of autoreactive T cells and enhanced ability to penetrate

the CNS. Thus, the markers of Table V include genes involved in perpetuating pathologic cellular proliferation and tissue destruction within the CNS characteristic of MS, along with increased resistance to regulation. This marker set accurately defines the requirements for an individual to develop MS, and thus has important predictive value, especially in diagnosing individuals having MS in the "probable" stage.

The identification of these markers significantly advances the field of MS diagnosis and treatment as well as provides tools which will enable elucidation of the mechanisms underlying MS formation and progression, ultimately leading to formulation of efficient, stage specific, treatment regimens.

The markers of the invention may be nucleic acid molecules (e.g., DNA, cDNA, or RNA) or the polypeptides encoded thereby. As such, detection of markers in a sample obtained from an individual can be effected using various detection methods well known to the ordinary skilled artisan.

Briefly, measurement of the relative amount of nucleic acid or polypeptide molecules can be effected by any method known in the art (see, e.g., Sambrook, J., Fritsh, E. F., and Maniatis, T. Molecular Cloning: A Laboratory Manual. 2nd, ed, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989; and Current Protocols in Molecular Biology, eds. Ausubel et al. John Wiley & Sons: 1992). Typical methodologies for RNA detection include RNA extraction from a cell or tissue sample, followed by hybridization of a labeled probe (e.g., a complementary nucleic acid molecule) specific for the target RNA to the extracted RNA, and detection of the probe (e.g., Northern blotting). Typical methodologies for polypeptide detection include activity assays in cases of known enzymes, protein extraction from a cell or tissue sample, followed by hybridization of a labeled probe (e.g., an antibody) specific for the target protein to the protein sample, and detection of the probe. The label group can

be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Detection of specific polypeptide and nucleic acid molecules may also be assessed by gel electrophoresis, column chromatography, direct sequencing, or quantitative PCR (in the case of nucleic acid molecules) among many other techniques well known to those skilled in the art.

Probes based on the nucleotide sequence of a marker gene or of a nucleic acid molecule encoding a marker polypeptide of the invention can be used to detect transcripts or genomic sequences corresponding to the marker gene(s) and/or marker polypeptide(s) of the invention. In preferred embodiments, the probe comprises a label group attached thereto, e.g., the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissue which misexpress (e.g., over- or under-express) a marker polypeptide of the invention, or which have greater or fewer copies of a marker gene of the invention. For example, a level of a marker polypeptide-encoding nucleic acid in a sample of cells from a subject may be detected, the amount of mRNA transcript of a gene encoding a marker polypeptide may be determined, or the presence of mutations or deletions of a marker gene of the invention may be assessed. The invention further encompasses nucleic acid molecules that differ from the nucleic acid sequences of the genes set forth in Tables I-V, due to degeneracy of the genetic code and which thus encode the same proteins as those encoded by the genes shown in Tables I-V.

An isolated marker protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind marker proteins using standard techniques for polyclonal and monoclonal antibody preparation. A full-length marker protein can be used or, alternatively, the invention provides antigenic peptide fragments of these proteins for use as immunogens. The antigenic peptide of a marker protein comprises at least 8 amino acid residues of an amino acid sequence encoded by a gene set forth in Tables I-V, and

encompasses an epitope of a marker protein such that an antibody raised against the peptide forms a specific immune complex with the marker protein. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the marker protein that are located on the surface of the protein, e.g., hydrophilic regions, as well as regions with high antigenicity.

An anti-marker protein antibody (e.g., monoclonal antibody) can be used to isolate a marker protein of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-marker protein antibody can facilitate the purification of natural marker proteins from cells and of recombinantly produced marker proteins expressed in host cells. Moreover, an anti-marker protein antibody can be used to detect marker protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the marker protein. Anti-marker protein antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase,

luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (J. Mol. Biol. 1990;215:403-10). BLAST nucleotide searches can be performed with the NBLAST program, score=100, wordlength=12 to obtain nucleotide sequences homologous to nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to marker protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) Nucleic Acids Res. 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See http://www.ncbi.nlm.nih.gov.

It will be appreciated that non-coding sequences, such as promoter or other regulatory sequences of marker genes may be used as probes in the context of the present invention. Thus, the expression of groups of functionally related genes, responsive to similar signals important to the pathogenesis or progression of multiple sclerosis, may be assessed.

It will be appreciated that in certain cases the genes themselves can serve as markers. For example, mutations in the nucleic acid sequence of a gene (e.g., non-sense, mis-sense deletion and the like) which result in lower expression levels of the gene or lower activity of the gene product may be correlated with MS. Similarly, a duplication of the gene, which can result in higher expression levels or mutations which result in higher activity can also be correlated with MS.

Detection of the presence or number of copies of all or a part of a marker gene of the invention may be performed using any method known in the art. Typically, it is convenient to assess the presence, quantity and quality of genomic DNA by Southern analysis, in which total DNA from a cell or tissue sample is extracted, is hybridized with a labeled probe (e.g., a complementary DNA molecule), and the probe is detected. The label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Other useful methods of DNA detection and/or quantification include direct sequencing, gel electrophoresis, column chromatography, and quantitative PCR, as is known by one skilled in the art.

In cases where detection involves discrete marker sets, the detection method of the present invention preferably employs marker probes which are conjugated to a solid support. For example, polynucleotide probes capable of specifically hybridizing with polynucleotide markers of the present invention (e.g., mRNA) may be coupled to an array (e.g., a GeneChip array for hybridization analysis), to a resin (e.g., a resin which can be packed into a column for column chromatography), or a matrix (e.g., a nitrocellulose matrix for northern blot analysis). The immobilization of molecules complementary to the marker(s), either covalently or noncovalently, permits a discrete analysis of the presence or activity of each marker in a sample. In an array, for example, polynucleotides complementary to each member of a marker set may individually be attached to different, known locations on the array (region-specific arrays). The array may be hybridized with, for example, polynucleotides extracted from a blood sample obtained from a subject. The hybridization of polynucleotides extracted from the sample with the array at any location on the array can be detected, and thus the presence or quantity of the marker in the sample can be ascertained. In a preferred embodiment, a "GeneChip" array is employed (e.g., an Affymetrix type array). Similarly, Western analyses may be performed on immobilized antibodies specific for

different polypeptide markers hybridized to a protein sample from a subject.

It will also be apparent to one skilled in the art that the probes of the array need not bind with the entire marker molecule. A probe designed to bind a portion of the marker of sufficient length for detection purposes (e.g., for hybridization), for example, a portion of the marker which is 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 100 or more nucleotides or amino acids in length may be sufficient for detection purposes.

Polynucleotide probes can be synthesized using any known synthesis method. Preferably, synthesis is effected using on-chip lithography methodology in a manner similar to that utilized for the synthesis of Affymetrix chips (www.affymetrix.com). Additional methods of array production and methodology are described in detail in the U.S. Patent Applications cited in the Background section hereinabove.

Antibody probes useful for detecting polypeptide markers can be generated using various well known techniques. For example, monoclonal antibodies which can be used per se or as a basis for antibody fragments (scFv, Fab etc) can be synthesized using isolated Hybridomas. In such an approach, a protein corresponding to a marker of the invention is isolated (e.g., by purification from a cell in which it is expressed or by transcription and translation of a nucleic acid encoding the protein in vivo or in vitro using known methods. A vertebrate, preferably a mammal such as a mouse, rat, rabbit, or sheep, is immunized using the isolated protein or protein fragment. The vertebrate may optionally (and preferably) be immunized at least one additional time with the isolated protein or protein fragment, so that the vertebrate exhibits a robust immune response to the protein or protein fragment. Splenocytes are isolated from the immunized vertebrate and fused with an immortalized cell line to form hybridomas, using any of a variety of methods well known in the art. Hybridomas formed in this manner are then screened

using standard methods to identify one or more hybridomas which produce an antibody which specifically binds with the protein or protein fragment.

The invention also includes an array comprising a marker(s) of the present invention. The array can be used to assay expression of one or more genes in the array.

In one embodiment, the array can be used to assay gene expression in a tissue of multiple sclerosis patients at different stages of the disease to ascertain stage specificity of genes in the array. In this manner, more than about 30,000 genes can be simultaneously assayed for expression. This allows a profile to be developed showing a battery of genes specifically expressed in one or more stages of the disease.

In addition to such qualitative determination, the invention allows the quantitation of gene expression. Thus, not only stage specificity, but also the level of expression of a battery of stage specific genes is ascertainable. Thus, genes can be grouped on the basis of their expression per se, and level of expression in that stage of the disease.

The detection arrays described herein are preferably packaged in kits identified for use in detecting MS in general or for detecting specific stages of MS. The kit can further include reagents suitable for the detection of polynucleotide hybridization or antibody binding and instructions for effecting diagnosis using the kit components and suitable detection hardware (e.g., detection microscope) and software (e.g., detection and analysis software). For further description of such hardware and software and detection reagents please see www.affymetrix.com.

Thus, the present invention provides methods useful for diagnosing MS including specific stages or states of the disease and also a risk of developing the disease.

These methods involve isolating a sample from a subject (e.g., a sample containing T-cells), detecting the presence, quantity, and/or activity of one or

more markers of the invention in the sample relative to a normal sample. Observing a significant increase or decrease in one or more markers in the test sample indicates the presence or risk of presence of MS.

Using specific marker sets, the present invention also provides methods of assessing the severity or stage of MS in a subject.

As detailed hereinabove, a major concern in treatment of multiple sclerosis is accurate early diagnosis following the first acute attack. At present, clinical studies indicate that only 40-50% of individuals suffering a first acute attack will progress to clinically definite MS. Thus, treatment protocols most commonly suspend treatment of these patients defined as probable MS, until the appearance of a second attack, which may entail years of waiting and uncertainty. It will be appreciated that early and accurate detection of the portion of probable MS patients likely to progress to further stages of the disease can save undue suffering and expense, and, more importantly, provide early treatment and a better prognosis for the portion of probable MS patients likely to progress to more severe stages. The present invention provides, for the first time, marker genes for probable MS, as well as for relapsing vs. remitting MS.

The present invention also provides methodology which can be used to assess the efficacy of an MS treatment regimen and/or the effect of environmental factors or diet on the progression of MS.

These methods involve isolating a sample from a subject (e.g., a sample containing T-cells) suffering from MS who is undergoing treatment which includes drug therapy, exposure to a predetermined environmental condition and/or a specific diet, detecting the presence, quantity, and/or activity of one or more markers of the invention in test samples obtained from the subject prior to and following treatment or in a test sample obtained from the subject relative to a sample obtained from an individual suffering from MS who is not undergoing any treatment and/or relative to a sample obtained from an individual not

suffering from MS and undergoing treatment. The levels of markers in the samples are compared, and significant increases or decreases in one or more markers in the test sample following treatment relative to the other samples are observed, and correlated with the severity or stage of MS. By assessing whether MS has been lessened or alleviated, the ability of the treatment or therapy to treat MS is also determined.

It will be appreciated that the present invention also provides methods of treating (e.g., inhibiting) the formation or progression of MS. These methods involve isolating a sample from a subject (e.g., a sample containing PMBCs such as T-cells), detecting the presence, quantity, and/or activity of one or more markers of the invention in the sample relative to a normal sample and observing significant increases or decreases in one or more markers in the test sample. For markers that are significantly decreased in expression or activity, the subject may be administered that expressed marker protein, or may be treated by the introduction of mRNA or DNA corresponding to the decreased marker (e.g., by gene therapy), to thereby increase the levels of the marker protein in the subject. For markers that are significantly increased in expression or activity, the subject may be administered mRNA or DNA antisense to the increased marker (e.g., by gene therapy), or may be administered antibodies specific for the marker protein, to thereby decrease the levels of the marker protein in the subject. In this manner, the subject may be treated for MS or MS related condition.

In another embodiment, the methods further involve obtaining a control biological sample (e.g., nondiseased tissue) from a control subject, contacting the control sample with a compound or agent capable of detecting marker protein, mRNA, or genomic DNA, such that the presence of marker protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of marker protein, mRNA or genomic DNA in the control sample

with the presence of marker protein, mRNA or genomic DNA in the test sample.

The invention also provides methods for identifying modulators, i.e., candidate or test compounds or agents (e.g., peptides, peptidomimetics, peptoids, small molecules or other drugs) which (a) bind to the marker, or (b) have a modulatory (e.g., stimulatory or inhibitory) effect on the activity of the marker or, more specifically, (c) have a modulatory effect on the interactions of the marker with one or more of its natural substrates (e.g., peptide, protein, hormone, co-factor, or nucleic acid), or (d) have a modulatory effect on the expression of the marker. Such assays typically comprise a reaction between the marker and one or more assay components. The other components may be either the test compound itself, or a combination of test compound and a natural binding partner of the marker. The test compounds of the present invention may be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. Test compounds may also be obtained by any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive; (see, e.g., Zuckermann et al., 1994, J. Med. Chem. 37:2678-85); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the `one-bead one-compound` library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, Anticancer Drug Des. 12:145).

Additional objects, advantages, and novel features of the present invention will become apparent to one ordinarily skilled in the art upon

examination of the following examples, which are not intended to be limiting. Additionally, each of the various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below finds experimental support in the following examples.

EXAMPLES

Reference is now made to the following examples, which together with the above descriptions, illustrate the invention in a non limiting fashion.

Generally, the nomenclature used herein and the laboratory procedures utilized in the present invention include molecular, biochemical, microbiological and recombinant DNA techniques. Such techniques are thoroughly explained in the literature. See, for example, "Molecular Cloning: A laboratory Manual" Sambrook et al., (1989); "Current Protocols in Molecular Biology" Volumes I-III Ausubel, R. M., ed. (1994); Ausubel et al., "Current Protocols in Molecular Biology", John Wiley and Sons, Baltimore, Maryland (1989); Perbal, "A Practical Guide to Molecular Cloning", John Wiley & Sons, New York (1988); Watson et al., "Recombinant DNA", Scientific American Books, New York; Birren et al. (eds) "Genome Analysis: A Laboratory Manual Series", Vols. 1-4, Cold Spring Harbor Laboratory Press, New York (1998); methodologies as set forth in U.S. Pat. Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057; "Cell Biology: A Laboratory Handbook", Volumes I-III Cellis, J. E., ed. (1994); "Culture of Animal Cells - A Manual of Basic Technique" by Freshney, Wiley-Liss, N. Y. (1994), Third Edition; "Current Protocols in Immunology" Volumes I-III Coligan J. E., ed. (1994); Stites et al. (eds), "Basic and Clinical Immunology" (8th Edition), Appleton & Lange, Norwalk, CT (1994); Mishell and Shiigi (eds), "Selected Methods in Cellular Immunology", W. H. Freeman and Co., New York (1980); available immunoassays are extensively described in the patent and scientific literature, see, for example, U.S. Pat. Nos. 3,791,932; 3,839,153; 3,850,752; 3,850,578;

3,853,987; 3,867,517; 3,879,262; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; 4,098,876; 4,879,219; 5,011,771 and 5,281,521; "Oligonucleotide Synthesis" Gait, M. J., ed. (1984); "Nucleic Acid Hybridization" Hames, B. D., and Higgins S. J., eds. (1985); "Transcription and Translation" Hames, B. D., and Higgins S. J., eds. (1984); "Animal Cell Culture" Freshney, R. I., ed. (1986); "Immobilized Cells and Enzymes" IRL Press, (1986); "A Practical Guide to Molecular Cloning" Perbal, B., (1984) and "Methods in Enzymology" Vol. 1-317, Academic Press; "PCR Protocols: A Guide To Methods And Applications", Academic Press, San Diego, CA (1990); Marshak et al., "Strategies for Protein Purification and Characterization - A Laboratory Course Manual" CSHL Press (1996); all of which are incorporated by reference as if fully set forth herein. Other general references are provided throughout this document. The procedures therein are believed to be well known in the art and are provided for the convenience of the reader. All the information contained therein is incorporated herein by reference.

MATERIALS AND METHODS

Subjects - Blood was obtained from patients or controls after written informed consent. *For comparison of healthy controls and MS patients, and between MS patients in acute relapse or remission*: Gene expression profiles of 26 patients (20 females, mean age 41.0±2.5 years) with definite diagnosis of MS according to Poser criteria (8), a relapsing-remitting disease course, and brain magnetic resonance imaging ascertaining the diagnosis (9) were compared with eighteen (18) age-matched healthy subjects (16 females). *For comparison of transcriptional profiles in MOG-reactive T-cells*: Four MS female patients (mean age 38±4.2 years, mean disease duration 9.3±3.3 years) having a definite MS according to Poser criteria (10), a relapsing-remitting disease course, neurological disability evaluated by the expanded disability status scale (EDSS, 11) between 2 to 5.0, and brain MRI supporting the

diagnosis of MS, and three age- and sex-matched healthy controls were included in the study. None of the patients received immunomodulatory drugs or steroid treatment for at least three months prior to when blood was drawn. The studies were approved by the institutional review board and the Israel Ministry of Health.

mRNA preparation - Total RNA was isolated from Ficoll™ isolated Peripheral Blood Mononuclear Cells (PBMC) or from MOG-stimulated T cell lines ($2x10^7$ cells) by ice-cold TRIZOL Reagent (Gibco, BRL). Poly-A mRNA was isolated using a mini-kit (Oligotex, Qiagen) and used as a template for double-stranded cDNA synthesis using oligo (dT)-24 primers containing a T7 RNA polymerase promoter site added to the 3'- end (Genset). After phenol/chloroform extraction cDNA was used as a template for *in vitro* transcription (Ambion T7 Megascript system) with biotin labeled nucleotides (Enzo Diagnostics). Labeled cRNA was fragmented, quantified by spectrophotometer, and hybridized to the microarrays.

Microarray gene analysis - Each Genechip (U95Av2) which carries probes for 12,625 (or U133A with 22,000 for patients with probable MS diagnosis) transcripts was hybridized with 10μg/200μl hybridization mix, stained and scanned (Hewlett Packard, GeneArray-TM scanner G2500A) according to manufacturer protocol (Affymetrix Inc, Santa Clara, CA). Scaling procedure was performed to an average intensity of 600 per gene. A value of 20 was assigned to all measurements lower then 20. *For comparison of healthy controls and MS patients, and between MS patients in acute relapse or remission*: All data was normalized by dChip software and fold ratios were calculated for each gene of the samples against geometric means of the matched controls. *For comparison of transcriptional profiles in MOG-reactive T-cells*: Genes that did not have at least one average difference intensity value $\geq$100 or were present at least once by Affymetrix criteria, were not included in the analysis.

Data analysis - The analysis was performed according to the analytical approach as previously described (24-26). Genechip 4 software (Affymetrix Inc, Santa Clara, CA) was used for analysis of the scanned arrays. Fold ratios were calculated for each gene of the samples against the geometric mean of matched controls. *For comparison of transcriptional profiles in MOG-reactive T-cells*: To determine the most informative genes threshold number of misclassifications (TNoM) score was applied. This score counts the number of classification errors that occur between compared groups for each gene of the dataset. The best threshold (TNoM=0) implies that no errors have been counted and the distinction between the two groups in relation to the expression level of a specific gene is maximal. To select a group of strongly differential expression, t-test p-value (comparing expression levels of genes from MS patients vs. healthy controls) were also computed. Genes with TNoM = 0, fold-change >1.5 (either up or down regulated) and corresponded t-test P value < 0.05, were designated as most informative. *For comparison of healthy controls and MS patients, and between MS patients in acute relapse or remission*: The data was analyzed by the classic parametric t-test, and the following non-parametric tests: (i) Threshold number of misclassifications (TNoM) method and (ii) INFO score that measures the misclassifications made by a simple threshold in terms of the information lost. Analysis was performed between MS patients and the control group for each gene of the dataset as well as between subgroups of patients. Only informative MS related genes ($p<0.05$ in all three statistical tests) were included. To retrieve the most informative genes, the False Discovery Rate (FDR) method (14) that ranks and tests all "P" values against different thresholds was used. The degree of significance by the Bonferroni threshold method, which evaluates the allowed error probability divided by the number of genes measured, and ensures that each and every validated scoring event is indeed a significant event, was also calculated.

Validation Strategy - To further assess the predictive power of the data sets, computerized analysis by the Leave-One-Out-Cross-Validation (LOOCV) statistical method was performed. The method simulates removal of a single sample every trial and trains on the rest. The procedure is repeated until each sample is left out once and the number of correct and incorrect predictions is counted.

EXAMPLE I

Accurate Gene Expression Profiles of MS

In order to provide an accurate, reliable profile of gene markers for diagnosis and evaluation of MS, DNA chip analysis was used to compare multiple gene expression patterns of PBMCs from patients with different clinical forms of MS. After informed consent blood was obtained from 26 patients (20 females, mean age 41.0±2.5 years) with definite diagnosis of MS according to Poser criteria, a relapsing-remitting disease course, and brain magnetic resonance imaging ascertaining the diagnosis. Eighteen age-matched healthy subjects (16 females) served as controls. PBMC gene expression of 12,625 human genes was analyzed as described hereinabove, using Ficoll™ for preparation of PBMCs and total RNA purification and sample preparation according to the instructions of Affymetrix, Inc (Affymetrix, Santa Clara CA, USA). In order to determine the most informative genes, unique computerized scoring methods, as yet not applied to analysis of data regarding MS, were employed. In brief, a gene is designated as informative based on the degree to which its tissue expression level is predictive of an independent classification of the tissue sample as "diseased" or "not diseased", as previously described by Ben-Dor et al (J Comput Biol 2000;7:559-63) and applied to the analysis of breast cancer and melanoma using cDNA arrays (for review see Freidman N et al Ernst Schering Res Found Wkshp 2002;38:109-31). The scores used in this study were:

TNoM (Total Number of Misclassifications) - the number of classification errors committed when using the best simple threshold to distinguish between two classes (diseased or not diseased) based on the expression levels of a specific gene.

INFO - an estimate of the uncertainty remaining about accuracy of a sample classification (diseased or not diseased) after the incorporation of

predictions based on expression of an individual gene is given (a lower "INFO" score indicates a higher predictive value for a given gene).

Gaussian (t-test) - The overlap between distributions of expression levels for genes in two classes. The score is based on normality assumptions.

One of the advantages of the analytic methods used here is their amenability to rigorous statistical benchmarking. Using this unique analysis, the number of informative genes per score expected in a random classification can be calculated, and then this estimated number of high scoring (or informative) genes can be compared to the actual number of informative genes (per score) measured in a dataset.

Comparison of the gene expression profiles shows that gene expression of PBMC in MS patients is significantly different from that in healthy subjects. Under the null-hypotheses that the separation of the samples is random despite genetic heterogeneity between tested groups, observed significant overabundance of informative genes was observed (Fig. 1A). The difference between expected and observed number of genes with significant p value in all 3 statistical tests (t-test, TNoM, INFO) performed, indicates that the diversity in gene expression observed in PBMC is biologically significant.

The predictive power of the data sets results was assessed by performing computerized error estimates based on *leave-one-out cross validation* (LOOCV) trials. The results disclosed only 3 classification errors. This low rate of error estimates suggest that the gene expression signature in MS is reliable for the diagnosis of the disease using peripheral blood and confirms that the patterns we observed accurately represent significant biologic phenomena associated with MS. The false discovery rate (FDR) method distinguished 1249 most informative genes that pass 95% FDR on all three statistical tests (t-test, TNoM, INFO) at $p < 0.05$ (Fig. 1B and Table I).

Confirmation of gene microarray expression findings was performed by RT-PCR for the following five randomly selected genes: EGFL5, P44, GS3686,

MX1 and CCR2. Significant correlations (coefficients ranged from 0.76 to 0.98) were found between the relative number of expression genes analysis and the RT-PCR profile. The data from microarray hybridizations was further tested against the strict Bonferroni threshold method from all three statistical tests, as described hereinabove, resulting in 300 top scoring genes that distinguish between MS and healthy subjects. (Table II).

The 1249 most informative genes (681 up-regulated, 569 down-regulated, Table I) consist of inflammatory, apoptosis and cell signaling pathways components, cytokines, antigen presentation molecules and chemokines as well as number of expressed sequence tags (ESTs).

Over-expressed genes in MS - The most abundant over-expressed transcripts unique to MS include: (i) **SLAM** (signaling lymphocyte activation molecule) a member of the immunoglobulin gene superfamily that is involved in T-cell stimulation. SLAM potentiates T-cell expansion and was described as CD28 independent co-stimulatory molecule, selectively increasing interferon gamma production and dysregulating type 1 and type 2 cytokine production in MS upon T-cell receptor activation. The surprising observation of SLAM upregulation suggests an enhanced proliferation of autoreactive T cells in MS patients; (ii) **LEF1** (lymphoid enhancer-binding factor 1) one of the transcriptional factors expressed in pre-B and T cells, and known to be associated with T cell receptor (TCR) stimulation and apoptosis survival of pro-B cells (19); (iii) **LRP5** (low density lipoprotein receptor-related protein 5) a of cell receptor protein required for LEF1 activation; (iv) **LILRB** (leukocyte immunoglobulin-like receptor), a protein that binds MHC class I molecules and delivers a negative signal inhibiting killing by natural killer and regulatory T cells; (v) **LY75** (lymphocyte antigen 75) an endocytotic receptor used by dendritic cells to direct captured antigens from the extracellular space to a specialized antigen-processing compartment; and (vi) **CDW52**, a 21-28 kDa glycopeptide antigen expressed on lymphocytes and macrophages known to be

a target for complement-mediated insult, inducing pro-inflammatory cytokine (e.g. TNF alpha and interferon gamma) production. Other up-regulated genes are members of the anti-apoptotic pathways, and include **PIP5K1-gamma** (Phosphatidylinositol-4-phosphate 5-kinase, type 1, gamma) and **MAP4** (Microtubule-associated protein 4). Over-expression of transcripts belonging to the papain cysteine proteinase family **CTSK** (Cathepsin K) and **CTSB** (Cathepsin B) was also observed.

Down-regulated genes in MS - Abundant down-regulated transcripts unique to MS that were identified include **IL1B** (Interleukin 1 beta), an important inflammatory cytokine; **TRAF6,** which is essential for IL1 signaling; and **SCYA20**, known to be mediated by IL1B. Decreased mRNA expression of **IL1B** was strengthened by the down regulation of **IL1R** (type1 receptor), **IL1RAP** (receptor accessory protein) and **IL1RN** (receptor antagonist).

Other important down-regulated genes include **TGFB1** (Transforming growth Factor beta 1) and **SKI** (v-ski sarcoma viral oncogene homologue) a component of TGFB signaling pathway, both known to inhibit cell proliferation. Thus, their under expression may contribute to autoreactive T cell expansion. Members of epidermal growth factor family such as **VEGF** (Vascular endothelial growth factor), **IGFBP4** (Insulin-like growth factor binding protein 4) and **EREG** (epiregulin) were also down regulated. Additionally, mRNA expression of members of the steroid-thyroid receptors family including nuclear receptor subfamily 4, group A members 1, 2 and 3 (**NR4A1, NR4A2, NR4A3**) were significantly reduced. Down regulation of these genes may inhibit apoptosis through Fas ligand and tumor necrosis factor alpha or through early response of T-cell receptor induced apoptosis of thymocytes, thus mimicking positive selection.

Taken together, the identification of profiles of up- (overexpressed) and down regulated genes specific to MS indicates the suitability of the methods of the present invention for identifying validated and significant molecular

signatures of PBMC gene expression in MS. While reducing the present invention to practice, it was observed that the specific disease related genes include transcripts involved in T cell activation and expansion and anti-apoptotic mediators, indicating failure of apoptosis-related elimination of autoreactive T cells.

EXAMPLE II

Stage Specific Gene Expression Profiles of MS

Accurate clinical tools for specific diagnosis of disease stages in MS are presently unavailable. In order to provide a useful profile of the clinically defined stages of MS, specific gene expression was evaluated in relation to clinical disease phases. Significant overabundance was found between the number of observed and expected genes expressed in MS patients during an acute relapse and in remission (Fig. 2A). Using the methods described hereinabove, the 743 most informative genes (302 up-regulated and 441 down-regulated) with p-value < 0.05 in all three scores (t-test, TNoM, INFO) that differentiated relapse from remission (Fig 2B, Table III) were identified.

Over-expressed genes in acute relapse of MS, compared to patients in remission - The most informative over-expressed genes included **CTSL** (Lysosomal cystein protease L, cathepsin L) known to play a role in MHC class II antigen presentation, responsible for quantitative and qualitative difference in peptide repertoires displayed by MHC class II molecules, and having a regulatory role in epitope generation for antigens subsets. Moreover, in vitro, proteolytic **CTSL** processed myelin basic protein into more then 60 different 20-40-mers species, and myelin-associated glycoprotein was described as a substrate for **CTSL** like proteases. These data, taken together with our observation that **CTSL** mRNA was over expressed in the active stage of MS, offer a biochemical basis for the immunodominant epitope spreading implicated in the pathogenesis of MS. Also up-regulated is **SCYA2** (Monocyte

specific chemoattractant protein, MCP1), essential for monocyte and NK cells recruitment to site of inflammatory injury. Augmented **SCYA2** expression level in the CNS has been identified at the onset of EAE. Other abundant up-regulated transcripts identified by the method of the present invention include **CD79A**, **DDIT3** (DNA-damage inducible transcript 3); **E2-EPF** (Ubiquitin carrier protein) and **COX6**.

Downregulated genes in acute relapse of MS, compared to patients in remission - From the downregulated gene transcripts in acute relapse vs. remission it is important to note several programmed cell death-related genes like **CCNG1** (Cyclin G1) identified as p53 dependent apoptosis; **PDCD2** (Programmed cell death 2) expressed in immature thymocytes; and **CTLA1** (Cytotoxic T lymphocyte associated serine esterase 1), crucial for the rapid induction of apoptosis by cytotoxic cells. Also prominently downregulated during acute relapse was **JAK1** (Janus kinase 1), a protein tyrosine kinase reported to be obligatory for several cytokines receptors, important for regulation of acute cellular response.

The results of the functional annotation of the transcriptional motifs that distinguish between acute MS relapse and remission suggest that many of the genes are involved in cellular recruitment and epitope spreading, as well as important to immunologic mechanisms related to escape from regulatory surveillance and augmentation of cell survival potential. Thus, it can be suggested that during the acute inflammatory process of the disease there is a failure of the immune regulatory cells to inhibit autoreactivity and the self-expansion of the non-restrained autoreactive T cells further lead to a vicious cycle of on going inflammatory activity.

It is evident from the gene-clustering map (Fig 2B) that during an acute relapse no significant differences are found between relapse treated vs. relapse untreated patients. Such a result is of great clinical significance, since this may indicate that during an acute MS exacerbation the major gene expression

transcripts are related to relapse associated genes and the effect of therapy is negligible. However, during remission treatment effect was more pronounced and this effect on gene suppression in treated patients was evident.

Of even greater significance is the demonstration, for the first time, of a specific gene expression profile of the "probable" stage of MS. As described hereinabove, "probable" MS precedes definitive clinical diagnosis, and is characterized by diverse neurological symptoms including unilateral loss of vision, true vertigo, ataxia, paresthesia, incontinence, diplopia, dysarthria or paralysis. Probable MS patients may suffer undiagnosed for years. In order to provide a method for accurate diagnosis of probable MS, in advance of onset of clinical symptoms, gene expression in PBMC samples of 13 probable MS patients were compared with that of samples from 5 age-matched healthy controls. RNA preparation, hybridization to MicroArray and analysis of results was performed as described for Examples 1 and 2, and in the Material and Methods section hereinabove.

As is shown in Table V, a specific "probable" MS profile of gene expression distinguishes PBMCs of diseased and healthy individuals.

Thus, there is demonstrated, for the first time, gene expression profiles providing criteria for distinguishing between stages of MS in humans, for example, between relapsing and remitting MS, probable MS and healthy individuals. Further, the groups of up- and down-regulated genes identified herein may be used for investigation of mechanisms of disease and disease progression in MS.

EXAMPLE III

Gene Expression Profiles in Treatment of MS

The effect of immunomodulatory treatment on gene expression in MS patients was investigated by comparison analysis of gene transcripts between treated and untreated patients. Suprisingly, despite the variety of

immunomodulatory treatments and differences between patients in relation to treatment duration, the microarray methods described herein, treatment-related gene transcripts that differentiated between treated and untreated patients were detected. Treatment-specific gene expression is mainly associated with phosphorylation and signal transduction. Thus, gene microarray technology can be a powerful tool in evaluating and monitoring clinical correlations of effects of treatment, and determining prognosis.

Thus, data presented herein demonstrate for the first time distinct and significant fingerprint cluster in MS patients that differentiates them from healthy subjects. Moreover, the stringent and specific fingerprint is predictive for the diagnosis of MS and is suitable for guiding the selection of patients for early treatment. Additionally, separate gene expression patterns were identified between acute MS relapse and remission, and treatment effects could also be identified. The methods described herein may also be used to offer superior insight into the biological mechanisms involved in the disease as well as improving functional gene characterization and transcription sites detection, important for identification of new targets for treatment and drug identification, such as T cell activation and expansion and anti-apoptotic genes like **SLAM**, **PIP5K1-g** and the **NR4A1-3** steroid-thyroid receptors subfamily.

EXAMPLE IV

Gene Expression Profiles of MOG-Reactive T-cells from MS Patients

Although MS appears to be caused by autoimmune T cells activated against myelin self-antigens, myelin-reactive T-cells have been demonstrated in healthy subjects as well. Thus, distinction between disease-related and non-disease related T-cell myelin reactivity is of great clinical and investigational importance. In order to determine a profile of MS-related T-cell genes, gene expression in MOG-reactive T-cells from 4 MS patients having relapsing-

remitting disease course, positive Poser criteria, and neurological disability, and 3 healthy age-matched controls was compared.

Using the microarray methods described herein, gene expression patterns obtained in MOG reactive T cell lines from MS patients detected 150 transcripts with TNoM=0, p=0.057 compared to healthy subjects (Figure 4). These high scoring gene transcripts were defined as significant MOG reactive MS-related genes. Hierarchical clustering of gene expression patterns from MS patients and healthy controls is presented in Figure 2, panel A. From the 150 genes with absolutely different expression levels, 43 most informative genes were further identified and clustered. These include 18 up-regulated and 25 down-regulated genes (Figure 2, panel B).

Investigation of the known biological function of these genes (Table V) shows a great diversity of activity (A Pie-chart diagram showing the functional groups of genes included in this evaluation is presented in Figure 3). Included are genes coding for proteins involved in the regulation and execution of apoptosis, growth factors, mediators of signal transduction pathways, molecules that participate in inflammation and also genes encoding heat shock proteins, transcription factors and components of different biochemical pathways.

Upregulated Genes in MS-Derived T-cells - Up-regulated in MS patient-derived T-cell lines are several anti-apoptotic genes such as **BCL2**, **lifeguard**, and the MAP-activated kinase **MAP3K12**. The **BCL2** gene product is an important member of the anti-apoptotic proteins. Lifeguard (**LFG**), is a molecule that inhibits cell death mediated by the Fas (CD95) receptor through a unique mechanism that down regulates apoptotic signals from Fas and is associated with human autoimmune lymphoproliferative syndrome (ALPS) and in lymphoproliferative lupus-like syndrome in mice.

The MAP3K12 gene is associated with programmed cell death and encodes a polypeptide that catalyzes the phosphorylation of BAD, a member of the BCL2 anti-apoptosis protein family. Increased expression of **IGFBP3** and

VEGF was also demonstrated in MS-derived T cells. **IGFBP-3** has been implicated in the expansion of disease related T-cell, associated with acute brain lesions of MS patients. Thus, in addition to increased survival potential, our findings suggest that autoreactive T cells in MS also have an expansion advantage compared with T cells from healthy individuals.

Furthermore, migration of autoimmune T cells into the brain would be expected to be assisted by over-expression of transcripts encoding for vascular endothelial growth factor (**VEGF**) in lines from MS patients. **VEGF** enhances vascular permeability and may facilitate migration of lymphocytes into the CNS and induction of inflammatory reactions in the brain.

Downregulated Genes in MS-Derived T-cells - The profile of gene expression in MS-derived T-cells (Figure 4, and Table V) indicates a suppression of apoptosis-related functions in the diseased state. One aspect of failure to induce apoptosis in the MS-derived T cell lines is the significant down-regulation of the gene encoding for the pro-apoptotic molecule **TNF**. A reduction in **TNF** could also contribute to a reduction in the ratio of pro- and anti-apoptotic transcript expression in the anti-MOG T cell lines from MS patients compared to healthy controls. Indeed, inadequate apoptosis present in MS autoreactive T cell lines could lead to insufficient deletion of autoimmune activated T cell clones and increase susceptibility to autoimmunity.

In addition, effectors of MHC class I presentation were revealed to be down-regulated in MS patients' cells. Such down-regulated expression includes the transcript for the **proteasome PA28 complex**, known to be a principal provider of MHC class I-presented peptides in antigen presenting cells, and **HSP70 1A and 1B** variants. **TNF** is also known to stimulate MHC class I presentation in addition to induction of apoptosis. The findings presented herein indicate that a weaker antigenic MHC class I presenting capability might distinguish MS-patient derived T cell lines from their healthy counterparts, and providing powerful diagnostic tools. It is conceivable that a lower expression of

MHC class-I on CD4 autoimmune T cells might enable them to escape regulation by CD8 cells that recognize autoimmune idiotypes.

Taken together the combined effects of down-regulation of apoptosis associated genes, up regulation of anti-apoptotic genes, increased expansion capability by autoreactive T cells and enhanced ability to penetrate the CNS may lead to perpetuated pathologic cellular proliferation and tissue destruction within the CNS characteristic of MS, along with increased resistance to regulation. The specific gene expression profiles described herein can define some of the requirements for an individual to develop MS, and thus have important predictive value, especially in determining MS in the "probable" stage. It is noteworthy that despite activation in vitro with the same MOG epitope, anti-MOG T cells from healthy subjects did not attain the gene expression profile that characterized the MS patient-derived cells. The findings support the concept that not all autoimmune T cells are equal; autoimmune T cells from MS patients follow a unique pattern of T cell activation that appears to be more resilient to apoptosis and can support long term survival. Although T cell lines derived from MS patients and healthy donors responded to the same autoantigen, were both activated T cell populations that proliferated extensively in the presence of IL-2, the gene expression imprints that are unique to each group were preserved. These findings indicate the existence of different T-cell activation mechanisms. The nature of the stimuli that generate aberrant autoimmune T-cell gene expression has yet to be identified in order to determine whether their formation is merely the result of the chronic immune stimulation driven by other factors in MS, or whether such T cells function as primary drivers of the MS process. Characterization of such driver T cells, dictating the state of immunity/autoimmunity can also greatly contribute to understanding autoimmunity and possibly also for designing effective treatments for MS.

ANNOTATED MARKED-UP SPECIFICATION

TABLES I-V

Table I: Gene Expression Profile from PBMCs of MS vs. Healthy

Affymetrix ID no:~~SEQ ID NO:~~	Identifier	TNOM PValue	Info PValue	t-Test PValue	Log Fold Change	Symbol
40289_at~~1~~	U78107	8.55E-11	1.94E-11	4.04E-12	-0.43769	NAPG
39402_at~~2~~	M15330	8.55E-11	8.55E-11	2.49E-12	-2.13825	IL1B
41499_at~~3~~	X15218	8.55E-11	8.55E-11	1.40E-10	-1.41501	SKI
1953_at~~4~~	AF024710	8.55E-11	8.55E-11	1.13E-12	-1.95537	VEGF
189_s_at~~5~~	U09937	1.84E-09	4.16E-10	2.04E-09	-1.21578	HSUROKR7
38873_at~~6~~	AB018343	1.84E-09	4.16E-10	9.05E-12	0.383078	KIAA0800
41169_at~~7~~	X74039	1.84E-09	4.16E-10	1.51E-10	-0.67381	PLAUR
242_at~~8~~	M64571	1.84E-09	1.84E-09	2.41E-11	0.416659	MAP4
40385_at~~9~~	U64197	1.84E-09	1.84E-09	2.95E-10	-0.62373	SCYA20
1983_at~~10~~	X68452	2.57E-08	2.93E-09	9.12E-11	-0.26618	CCND2
32133_at~~11~~	AB011161	2.57E-08	2.93E-09	9.64E-11	0.63432	PIP5K1C
37579_at~~12~~	L47738	2.57E-08	2.93E-09	7.54E-09	0.31646	PIR121
1209_at~~13~~	U78798	2.57E-08	2.93E-09	1.11E-06	-0.3172	TRAF6
40365_at~~14~~	M63904	2.57E-08	7.16E-09	5.38E-09	-0.59612	GNA15
35227_at~~15~~	U72066	2.57E-08	7.16E-09	4.33E-08	-0.34482	RBBP8
37936_at~~16~~	AI184802	2.64E-07	1.61E-08	2.67E-09	-0.21576	HPRP4P
41831_at~~17~~	AF077820	2.64E-07	1.61E-08	2.91E-08	0.656852	LRP5
279_at~~18~~	L13740	2.64E-07	1.61E-08	5.83E-08	-1.45891	NR4A1
39561_at~~19~~	AL008583	2.64E-07	1.61E-08	1.12E-08	0.250082	
34857_at~~20~~	Z24724	2.64E-07	1.61E-08	5.96E-09	-1.10426	
34476_r_at~~21~~	D30783	2.57E-08	2.19E-08	8.95E-10	-1.65011	EREG
34405_at~~22~~	U47927	2.57E-08	2.19E-08	5.53E-09	0.545592	USP5
32021_at~~23~~	AI560890	2.57E-08	2.19E-08	1.80E-07	0.179028	
37185_at~~24~~	Y00630	2.57E-08	3.69E-08	6.65E-09	-2.38485	SERPINB2
34210_at~~25~~	N90866	2.64E-07	8.23E-08	2.76E-08	0.304525	CDW52
36100_at~~26~~	AF022375	2.64E-07	8.23E-08	1.87E-11	-1.35847	VEGF
36680_at~~27~~	M24895	2.11E-06	1.08E-07	1.72E-08	0.476779	AMY2B
33598_r_at~~28~~	AF054176	2.11E-06	1.08E-07	6.47E-09	-0.58138	C1orf7
33943_at~~29~~	L20941	2.64E-07	1.08E-07	1.78E-06	-0.58618	FTH1
1125_s_at~~30~~	L05424	2.11E-06	1.08E-07	2.27E-09	-0.58081	HUMSCG19
39797_at~~31~~	AB002347	2.11E-06	1.08E-07	7.19E-10	0.371731	KIAA0349
41431_at~~32~~	AB023153	2.11E-06	1.08E-07	1.82E-08	0.895842	KIAA0936
40870_g_at~~33~~	AF069517	2.11E-06	1.08E-07	4.91E-07	0.399638	RBM6
32444_at~~34~~	X69392	2.64E-07	1.08E-07	1.10E-08	0.297444	RPL26
36060_at~~35~~	U51920	2.11E-06	1.08E-07	7.01E-08	-0.28142	SRP54
1139_at~~36~~	L22075	2.64E-07	1.71E-07	1.10E-08	-0.55736	GNA13
1520_s_at~~37~~	X04500	2.64E-07	1.71E-07	3.43E-10	-2.12121	IL1B
39417_at~~38~~	AB028951	2.64E-07	1.71E-07	8.78E-09	0.543028	KIAA1028
35926_s_at~~39~~	AF004230	2.64E-07	1.71E-07	3.06E-07	0.349166	LILRB1
35165_at~~40~~	AF070582	2.64E-07	1.71E-07	3.23E-08	-0.19773	MGC13033

39183_at41	X66363	2.64E-07	1.71E-07	6.53E-07	-0.24505	PCTK1
1603_g_at42	L33881	2.64E-07	1.71E-07	5.06E-08	-0.59585	PRKCI
33513_at43	U33017	2.64E-07	1.71E-07	5.20E-07	0.373581	SLAM
38983_at44	AJ007042	2.64E-07	1.71E-07	2.10E-07	0.170935	WHSC1
39755_at45	Z93930	2.64E-07	1.71E-07	2.42E-05	-0.39839	XBP1
37233_at46	AF079167	2.64E-07	1.71E-07	7.37E-10	-1.93249	
31472_s_at47	AF098641	2.64E-07	1.71E-07	1.56E-07	-0.41172	
1181_at48	HG3227-HT3404	2.64E-07	1.71E-07	1.68E-08	-0.25361	
38104_at49	U78302	2.64E-07	1.71E-07	2.41E-08	0.329878	
34707_at50	U91543	2.64E-07	2.49E-07	2.01E-07	0.478678	CHD3
33993_at51	M22919	2.64E-07	2.49E-07	9.52E-08	-0.81053	MYL6
41795_at52	AB029015	2.64E-07	2.49E-07	5.37E-09	0.695063	PLCE2
37535_at53	Z11697	1.37E-05	4.08E-07	3.55E-06	-1.21033	CD83
32033_at54	AL096780	1.37E-05	4.08E-07	2.13E-06	0.34487	CHKL
32539_at55	U51205	1.37E-05	4.08E-07	2.65E-07	-0.76279	COP9
35935_g_at56	Y08683	1.37E-05	4.08E-07	4.71E-06	0.492738	CPT1B
32962_at57	S52028	2.11E-06	4.08E-07	9.62E-08	-0.81662	CTH
37365_at58	X63368	2.11E-06	4.08E-07	2.30E-08	-0.55432	DNAJB2
37825_at59	M84443	1.37E-05	4.08E-07	4.08E-07	0.303567	GALK2
496_s_at60	U32324	1.37E-05	4.08E-07	3.21E-08	0.334966	IL11RA
41077_at61	AB011115	1.37E-05	4.08E-07	3.39E-07	0.382809	KIAA0543
38854_at62	AB014535	1.37E-05	4.08E-07	1.04E-06	0.285282	KIAA0635
41485_at63	X02152	1.37E-05	4.08E-07	4.63E-08	-0.75601	LDHA
37819_at64	AF007130	2.11E-06	4.08E-07	2.51E-06	0.391811	LOC54104
35273_at65	AF007151	1.37E-05	4.08E-07	3.25E-06	0.468343	MMS19L
37283_at66	X82209	2.11E-06	4.08E-07	1.37E-09	-0.45281	MN1
38064_at67	X79882	1.37E-05	4.08E-07	1.78E-07	0.520965	MVP
38275_at68	U91616	1.37E-05	4.08E-07	1.27E-07	-0.80419	NFKBIE
38911_at69	U41815	1.37E-05	4.08E-07	2.16E-07	-0.96931	NUP98
32784_at70	AB011108	1.37E-05	4.08E-07	4.39E-07	0.453498	PRP4
36312_at71	L40377	1.37E-05	4.08E-07	3.49E-07	-0.79409	SERPINB8
39159_at72	X99656	1.37E-05	4.08E-07	1.68E-06	-0.23553	SH3GL1
40723_at73	AJ010059	2.11E-06	4.08E-07	2.95E-06	0.2235	SIT
33803_at74	J02973	1.37E-05	4.08E-07	2.93E-07	-1.30804	THBD
32715_at75	N90862	1.37E-05	4.08E-07	3.28E-08	0.43576	VAMP8
40729_s_at76	Y14768	1.37E-05	4.08E-07	7.26E-08	0.248383	
37723_at77	U47414	2.11E-06	7.73E-07	2.31E-06	0.370736	CCNG2
32259_at78	AB002386	2.11E-06	7.73E-07	5.34E-09	0.586117	EZH1
38429_at79	U29344	2.11E-06	7.73E-07	2.35E-07	-0.43842	FASN
35450_s_at80	AF015553	2.11E-06	7.73E-07	2.61E-07	0.61214	GTF2I
37571_at81	AB028981	2.11E-06	7.73E-07	5.34E-07	0.282288	KIAA1058
197_at82	U29656	2.11E-06	7.73E-07	7.52E-08	0.353186	NME3
430_at83	X00737	2.11E-06	7.73E-07	5.21E-08	-0.67074	NP
36159_s_at84	U29185	2.11E-06	7.73E-07	1.56E-07	-1.08006	PRNP
39691_at85	AB007960	2.11E-06	7.73E-07	7.96E-06	0.447772	SH3GLB1

162_at86	U44839	2.11E-06	7.73E-07	2.54E-07	-0.97008	USP11
38252_s_at87	U84007	7.44E-05	1.28E-06	0.000235	0.236422	AGL
1347_at88	S78187	7.44E-05	1.28E-06	1.95E-05	0.203265	CDC25B
38466_at89	X82153	7.44E-05	1.28E-06	2.27E-06	0.47844	CTSK
41336_at90	AL050084	7.44E-05	1.28E-06	5.26E-05	0.509331	DC8
32716_at91	X62535	1.37E-05	1.28E-06	5.68E-07	0.243937	DGKA
38556_at92	AB026436	7.44E-05	1.28E-06	0.000219	-0.7589	DUSP10
41426_at93	M98833	7.44E-05	1.28E-06	1.52E-06	0.434288	FLI1
33191_at94	AW051579	1.37E-05	1.28E-06	7.58E-07	0.593476	FLJ10512
40263_at95	X16706	7.44E-05	1.28E-06	1.23E-06	-1.09747	FOSL2
41323_at96	U90917	1.37E-05	1.28E-06	3.89E-07	0.433406	FOXM1
34609_g_at97	M24194	7.44E-05	1.28E-06	4.38E-06	0.560895	GNB2L1
39392_at98	AJ002190	7.44E-05	1.28E-06	2.17E-08	0.33775	GNPAT
36614_at99	X87949	7.44E-05	1.28E-06	4.05E-07	-0.54468	HSPA5
35303_at100	U96876	7.44E-05	1.28E-06	3.54E-06	-0.45317	INSIG1
38349_at101	AF038564	1.37E-05	1.28E-06	2.05E-07	-0.40446	ITCH
34034_at102	D80011	7.44E-05	1.28E-06	4.20E-07	-0.35073	KIAA0189
35851_g_at103	AI950382	1.37E-05	1.28E-06	1.63E-07	-0.74128	KIAA0585
36453_at104	AB023235	7.44E-05	1.28E-06	1.43E-05	0.311216	KIAA1018
36862_at105	AB029038	7.44E-05	1.28E-06	7.62E-05	0.364386	KIAA1115
33456_at106	U24166	7.44E-05	1.28E-06	7.52E-06	-0.45293	MAPRE1
40362_at107	X61498	7.44E-05	1.28E-06	8.80E-07	-0.49884	NFKB2
190_at108	U12767	7.44E-05	1.28E-06	2.84E-07	-1.23483	NR4A3
35741_at109	U85245	7.44E-05	1.28E-06	4.57E-07	0.365266	PIP5K2B
38120_at110	U50928	7.44E-05	1.28E-06	4.72E-06	0.302213	PKD2
525_g_at111	U13695	7.44E-05	1.28E-06	1.11E-05	0.805607	PMS1
32213_at112	AA203527	1.37E-05	1.28E-06	1.18E-07	0.281992	RPP20
38029_at113	J02939	7.44E-05	1.28E-06	2.16E-07	-0.87844	SLC3A2
40885_s_at114	N30151	7.44E-05	1.28E-06	5.05E-05	0.393521	STX16
34356_at115	U52960	2.11E-06	1.28E-06	1.51E-07	-0.84863	SURB7
32756_at116	AF030249	1.37E-05	1.28E-06	1.98E-07	0.534547	
40721_g_at117	AL022398	7.44E-05	1.28E-06	8.09E-08	0.919627	
1877_g_at118	HG1103-HT1103	1.37E-05	1.28E-06	1.16E-07	-0.39165	
37411_at119	D30758	2.11E-06	1.80E-06	1.58E-05	0.27738	CENTB1
31935_s_at120	U75968	2.11E-06	1.80E-06	4.36E-06	0.139542	DDX11
38326_at121	M69199	2.11E-06	1.80E-06	1.45E-07	-1.9021	G0S2
39781_at122	U20982	2.11E-06	1.80E-06	1.20E-08	-0.67125	IGFBP4
40493_g_at123	AF040707	2.11E-06	1.80E-06	3.57E-07	0.289845	NPR2L
32253_at124	AB007927	2.11E-06	1.80E-06	2.12E-07	0.323787	RERE
39388_at125	AA902713	2.11E-06	1.80E-06	1.44E-06	0.474378	
32106_f_at126	U66063	2.11E-06	2.24E-06	4.70E-07	0.277185	CAMK2G
41215_s_at127	D13891	2.11E-06	2.24E-06	4.57E-05	-0.20577	ID2
39976_at128	AL050087	2.11E-06	2.24E-06	1.27E-07	-0.31279	KIAA1785
35970_g_at129	N23137	2.11E-06	2.24E-06	2.06E-07	0.247311	MPHOSPH9
40564_at130	N42007	2.11E-06	2.24E-06	9.19E-05	0.167986	NUP50

ANNOTATED MARKED-UP SPECIFICATION

1231_at131	M74525	2.11E-06	2.24E-06	3.50E-07	-0.61792	UBE2B
37794_at132	AF035281	2.11E-06	2.24E-06	4.87E-07	0.472445	
38491_at133	U11732	1.37E-05	3.17E-06	3.04E-07	-0.22574	ETV6
34661_at134	AB002348	1.37E-05	3.17E-06	2.49E-07	0.576346	KIAA0350
40431_at135	AB007891	1.37E-05	3.17E-06	3.99E-05	0.196376	KIAA0431
39257_at136	AI754391	1.37E-05	3.17E-06	1.72E-06	-0.27657	KLF12
35234_at137	D50406	1.37E-05	3.17E-06	2.65E-05	0.461907	RECK
35142_at138	AF070617	1.37E-05	3.17E-06	3.23E-07	0.323494	
39791_at139	M23114	2.11E-06	4.08E-06	1.59E-07	-0.96141	ATP2A2
1445_at140	AF014958	2.11E-06	4.08E-06	1.05E-07	-0.42152	CCRL2
36639_at141	AF067853	1.37E-05	4.31E-06	5.02E-06	0.361707	ADSL
1252_at142	M73547	1.37E-05	4.31E-06	9.20E-08	0.438897	D5S346
39296_at143	W28319	1.37E-05	4.31E-06	1.50E-05	0.294631	FBLN1
39650_s_at144	AB007895	1.37E-05	4.31E-06	9.61E-07	0.186643	KIAA0435
35317_at145	AB014579	1.37E-05	4.31E-06	6.08E-08	0.367966	MGEA5
31675_s_at146	AF019083	1.37E-05	4.31E-06	8.34E-07	0.17011	PTENP1
38859_at147	AL080141	1.37E-05	4.31E-06	2.42E-07	0.330868	SEC31B-1
33810_at148	AF110377	1.37E-05	4.31E-06	3.05E-05	0.361232	TRRAP
36260_at149	AB002448	1.37E-05	4.31E-06	2.45E-07	0.468926	
34239_at150	AL049787	1.37E-05	4.31E-06	7.11E-06	0.311278	
1527_s_at151	U50527	1.37E-05	4.31E-06	5.11E-06	0.416543	
33588_at152	Z32860	1.37E-05	4.31E-06	7.81E-06	0.133192	
39562_at153	AF094481	1.37E-05	5.01E-06	2.74E-07	-0.29045	CGGBP1
493_at154	U29171	1.37E-05	5.01E-06	1.10E-06	-0.6032	CSNK1D
38296_at155	AL050196	1.37E-05	5.01E-06	2.00E-05	-0.24688	DKFZP586D2223
1788_s_at156	U48807	1.37E-05	5.01E-06	4.97E-08	-0.93178	DUSP4
37938_at157	U15552	1.37E-05	5.01E-06	1.67E-05	-0.68094	HSU15552
280_g_at158	L13740	1.37E-05	5.01E-06	9.10E-08	-0.61928	NR4A1
36079_at159	AF010309	1.37E-05	5.01E-06	7.36E-07	-0.28533	PIG3
38518_at160	Y18004	1.37E-05	5.01E-06	4.19E-07	-0.9465	SCML2
34779_at161	R90942	1.37E-05	5.01E-06	1.05E-05	-0.17696	ST6GALNACIV
33328_at162	W28612	1.37E-05	5.01E-06	1.70E-06	-0.25519	
40881_at163	X64330	7.44E-05	6.03E-06	2.27E-06	0.297851	ACLY
37229_at164	U49844	7.44E-05	6.03E-06	3.67E-07	0.47168	ATR
37760_at165	AB015019	7.44E-05	6.03E-06	2.75E-07	-0.24515	BAIAP2
39231_at166	AF006513	0.000344	6.03E-06	4.48E-05	-1.45973	CHD1
806_at167	U56998	0.000344	6.03E-06	3.70E-06	-0.74294	CNK
32065_g_at168	S68134	0.000344	6.03E-06	8.37E-07	-1.64652	CREM
32065_at169	S68134	0.000344	6.03E-06	4.35E-06	-2.47105	CREM
32067_at170	S68271	0.000344	6.03E-06	3.03E-06	-2.07185	CREM
38974_at171	AF021819	0.000344	6.03E-06	4.41E-05	0.298771	DJ-1
38628_at172	AF029777	1.37E-05	6.03E-06	8.27E-07	0.290159	GCN5L2
37706_at173	U28811	0.000344	6.03E-06	1.33E-06	0.32855	GLG1
1237_at174	S81914	0.000344	6.03E-06	4.18E-07	-1.59146	IER3
35116_at175	X80821	0.000344	6.03E-06	8.51E-05	-0.5606	KIAA0874

1774_at176	L06895	7.44E-05	6.03E-06	1.12E-05	-0.1928	MAD
40661_at177	D78579	1.37E-05	6.03E-06	4.25E-07	-1.65638	NR4A3
40662_g_at178	D78579	7.44E-05	6.03E-06	9.62E-07	-1.61438	NR4A3
40659_at179	U12767	0.000344	6.03E-06	2.55E-07	-2.13744	NR4A3
210_at180	M95678	0.000344	6.03E-06	2.00E-06	0.432923	PLCB2
31860_at181	X51804	0.000344	6.03E-06	7.23E-05	-0.19283	PMI
36856_at182	W28743	0.000344	6.03E-06	2.78E-06	-0.28926	PP1628
32227_at183	X17042	7.44E-05	6.03E-06	6.64E-06	-0.36481	PRG1
32186_at184	M80244	0.000344	6.03E-06	2.72E-06	-0.8522	SLC7A5
31888_s_at185	AF001294	1.37E-05	6.03E-06	1.23E-06	-0.76359	TSSC3
38523_f_at186	D49677	7.44E-05	6.03E-06	4.18E-06	0.198707	U2AF1RS2
41242_at187	AB011004	0.000344	6.03E-06	1.41E-06	-1.34073	UAP1
41430_at188	AB011113	1.37E-05	6.03E-06	3.74E-07	0.444795	WDR7
41488_at189	AC002394	0.000344	6.03E-06	0.001473	0.17105	
34338_at190	AL021707	0.000344	6.03E-06	4.95E-06	-2.21462	
40720_at191	AL022398	7.44E-05	6.03E-06	1.10E-07	0.79713	
40349_at192	AL049442	0.000344	6.03E-06	8.09E-06	0.621935	
36920_at193	U17760	0.000344	6.03E-06	4.25E-06	-0.84472	
32372_at194	L22569	1.37E-05	8.66E-06	1.52E-06	0.318129	CTSB
36138_at195	AL031058	1.37E-05	8.66E-06	0.000375	0.149046	DSP
41406_at196	AL080172	1.37E-05	8.66E-06	1.89E-05	0.098968	FLJ21919
34022_at197	M36821	1.37E-05	8.66E-06	2.21E-07	-0.36334	GRO3
39823_at198	U06631	1.37E-05	8.66E-06	1.31E-05	0.486332	H326
37497_at199	L16499	1.37E-05	8.66E-06	5.12E-06	0.374296	HHEX
41265_at200	X53586	1.37E-05	8.66E-06	3.40E-07	0.51291	ITGA6
35030_at201	D87466	1.37E-05	8.66E-06	1.49E-07	0.466046	KIAA0276
39551_at202	N98667	1.37E-05	8.66E-06	3.38E-07	0.367127	KIAA1696
32320_at203	X99142	1.37E-05	8.66E-06	1.24E-06	-0.29773	KRTHB6
38160_at204	AF011333	1.37E-05	8.66E-06	1.55E-05	0.342503	LY75
40138_at205	U70735	1.37E-05	8.66E-06	1.82E-06	0.249185	MOV34-34KD
33849_at206	U02020	1.37E-05	8.66E-06	1.37E-06	-1.13863	PBEF
40137_at207	M31724	1.37E-05	8.66E-06	0.000172	-0.2601	PTPN1
32579_at208	U29175	1.37E-05	8.66E-06	1.90E-06	0.266342	SMARCA4
36894_at209	AL031846	1.37E-05	8.66E-06	0.000418	0.38404	
39093_s_at210	Y12059	7.44E-05	1.51E-05	5.64E-06	-0.46008	BRD4
32977_at211	U49187	7.44E-05	1.51E-05	1.48E-06	0.671467	C6orf32
424_s_at212	X66945	7.44E-05	1.51E-05	1.91E-07	-0.35494	FGFR1
32181_at213	M60922	7.44E-05	1.51E-05	4.47E-08	0.39657	FLOT2
36021_at214	AL049409	7.44E-05	1.51E-05	1.10E-06	0.714173	LEF1
35434_at215	L16794	7.44E-05	1.51E-05	2.23E-05	-0.27553	MEF2D
1652_at216	U77735	7.44E-05	1.51E-05	5.66E-06	0.574142	PIM2
39734_at217	U10117	7.44E-05	1.51E-05	4.07E-06	0.563673	SCYE1
31410_at218	AF023614	1.37E-05	1.51E-05	4.79E-07	-0.20744	TACI
31508_at219	S73591	1.37E-05	1.51E-05	4.68E-06	0.414777	VDUP1
34962_at220	AF052160	7.44E-05	1.51E-05	1.67E-06	0.623021	
642_s_at221	L76528	7.44E-05	1.51E-05	6.14E-06	-0.39652	

39749_at222	U51007	7.44E-05	1.51E-05	1.49E-06	0.309996	
32567_at223	D10704	1.37E-05	1.75E-05	4.69E-07	-0.36791	CHK
40607_at224	U97105	1.37E-05	1.75E-05	6.56E-07	1.00615	DPYSL2
554_at225	U03634	1.37E-05	1.75E-05	1.00E-06	-0.21467	LBC
39037_at226	L13773	1.37E-05	1.75E-05	6.44E-07	0.247919	MLLT2
1373_at227	M31523	1.37E-05	1.75E-05	2.09E-06	0.36898	TCF3
37189_at228	AL023553	1.37E-05	1.75E-05	2.51E-06	0.226635	
32130_at229	W25984	7.44E-05	2.35E-05	1.42E-05	0.482493	ACTA1
36586_at230	U78521	0.000344	2.35E-05	2.53E-05	0.320909	AIP
34898_at231	M30704	0.000344	2.35E-05	1.65E-05	-0.37795	AREG
35765_at232	X91504	0.001377	2.35E-05	0.00016	0.233217	ARFRP1
32563_at233	U51478	7.44E-05	2.35E-05	6.10E-07	-0.58	ATP1B3
38201_at234	U21551	0.001377	2.35E-05	7.60E-05	-0.3088	BCAT1
40790_at235	AB004066	0.000344	2.35E-05	6.57E-05	-0.60905	BHLHB2
2036_s_at236	M59040	0.001377	2.35E-05	2.82E-06	-0.46271	CD44
40610_at237	M91670	0.001377	2.35E-05	0.001649	-0.47538	E2-EPF
38863_at238	U43774	0.000344	2.35E-05	8.80E-07	-0.39938	FCAR
41177_at239	AW024285	0.000344	2.35E-05	6.99E-06	-0.42098	FLJ12443
40615_at240	AA780049	7.44E-05	2.35E-05	7.39E-07	0.54912	FLJ21439
36484_at241	AI935146	0.000344	2.35E-05	2.05E-06	-0.46726	GALNT3
35289_at242	AJ011679	0.001377	2.35E-05	4.67E-05	0.243248	GAPCENA
34724_at243	AI670100	7.44E-05	2.35E-05	7.70E-07	0.22677	GRLF1
40113_at244	D87119	7.44E-05	2.35E-05	1.80E-06	0.425625	GS3955
31977_at245	M92432	0.000344	2.35E-05	4.31E-05	0.363033	GUCY2D
38771_at246	D50405	0.001377	2.35E-05	0.000688	0.387926	HDAC1
1636_g_at247	U07563	7.44E-05	2.35E-05	4.91E-07	-0.25016	HSABLGR3
37679_at248	Y10313	0.001377	2.35E-05	0.003201	-0.35345	IFRD1
33281_at249	D63485	0.000344	2.35E-05	9.04E-05	0.31177	IKKE
41524_at250	L08488	0.000344	2.35E-05	7.54E-06	-0.37883	INPP1
39753_at251	X06256	1.37E-05	2.35E-05	4.89E-07	-0.7357	ITGA5
37619_at252	D42084	0.001377	2.35E-05	7.39E-06	0.222195	KIAA0094
39783_at253	D43947	7.44E-05	2.35E-05	0.000104	0.269941	KIAA0100
40013_at254	AB007870	0.000344	2.35E-05	0.000108	-0.64362	KIAA0410
35850_at255	AI950382	0.000344	2.35E-05	0.000122	-0.65985	KIAA0585
34353_at256	AB014548	7.44E-05	2.35E-05	2.77E-05	0.431229	KIAA0648
31909_at257	AB018297	0.001377	2.35E-05	0.000836	0.195704	KIAA0754
34751_at258	AI970189	0.000344	2.35E-05	6.16E-07	-0.75934	KIAA0997
39057_at259	L04733	0.001377	2.35E-05	8.84E-07	0.306455	KNS2
1857_at260	AF010193	7.44E-05	2.35E-05	1.26E-07	-1.4705	MADH7
36126_at261	U18919	7.44E-05	2.35E-05	1.05E-05	0.271231	NBP
40823_s_at262	U85430	0.001377	2.35E-05	0.000315	0.317554	NFATC3
544_at263	S76638	7.44E-05	2.35E-05	7.47E-07	-0.35416	NFKB2
36963_s_at264	AL050353	0.000344	2.35E-05	4.42E-06	0.179352	OIP2
33705_at265	L20971	0.001377	2.35E-05	0.00089	-0.49725	PDE4B
41281_s_at266	AF060502	7.44E-05	2.35E-05	0.000114	-0.18239	PEX10
36480_at267	X80497	0.001377	2.35E-05	0.000245	0.313262	PHKA2

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38090_at268	AL050371	0.000344	2.35E-05	3.70E-06	0.493288	PISD
33543_s_at269	U77718	7.44E-05	2.35E-05	6.60E-06	0.352996	PNN
39747_at270	U52427	0.001377	2.35E-05	0.000282	0.329478	POLR2G
34914_at271	U94778	0.000344	2.35E-05	1.18E-05	0.282929	PSTPIP1
843_at272	U48296	0.001377	2.35E-05	0.00011	-0.89871	PTP4A1
1491_at273	M31166	0.001377	2.35E-05	0.000256	-0.38484	PTX3
35152_at274	AJ001016	7.44E-05	2.35E-05	1.08E-05	-0.28245	RAMP3
39847_at275	AF040965	0.001377	2.35E-05	0.001101	-0.38591	RES4-25
36674_at276	J04130	0.000344	2.35E-05	3.02E-06	-0.62071	SCYA4
33143_s_at277	U81800	0.000344	2.35E-05	4.28E-05	-0.49523	SLC16A3
41592_at278	AB000734	0.001377	2.35E-05	0.000883	-0.58764	SSI-1
39779_at279	U38847	7.44E-05	2.35E-05	9.91E-07	0.222946	TARBP1
38473_at280	M63180	0.001377	2.35E-05	1.03E-05	-0.33301	TARS
33439_at281	D15050	0.001377	2.35E-05	0.000192	-1.12874	TCF8
1106_s_at282	M12959	7.44E-05	2.35E-05	1.61E-06	0.128482	TRA@
429_f_at283	X00734	0.001377	2.35E-05	0.000384	-0.34516	TUBB5
31882_at284	AJ001340	0.001377	2.35E-05	4.21E-05	0.181208	U3-55K
37729_at285	Y08614	0.001377	2.35E-05	6.92E-05	0.305659	XPO1
37842_at286	AF054589	0.000344	2.35E-05	1.98E-06	0.945394	
33734_at287	AL022398	7.44E-05	2.35E-05	2.40E-06	0.493166	
38990_at288	AL031178	7.44E-05	2.35E-05	3.18E-05	0.410068	
33687_at289	AL049782	7.44E-05	2.35E-05	7.66E-07	0.237794	
1171_s_at290	HG1471-HT3923	0.001377	2.35E-05	0.000519	0.203133	
706_at291	HG4582-HT4987	7.44E-05	2.35E-05	4.63E-07	-0.39588	
32061_at292	U96629	0.001377	2.35E-05	1.00E-04	0.277256	
37213_at293	D64110	7.44E-05	2.58E-05	7.49E-05	-0.51036	BTG3
32583_at294	J04111	7.44E-05	2.58E-05	0.000108	-1.60276	JUN
1895_at295	J04111	7.44E-05	2.58E-05	4.68E-05	-1.14014	JUN
41483_s_at296	X56681	7.44E-05	2.58E-05	0.000112	-0.48711	JUND
38031_at297	D21853	7.44E-05	2.58E-05	0.000403	-0.25594	KIAA0111
36925_at298	X80692	7.44E-05	2.58E-05	3.44E-05	-1.1939	MAPK6
545_g_at299	S76638	7.44E-05	2.58E-05	5.23E-05	-0.46026	NFKB2
33863_at300	U65785	7.44E-05	2.58E-05	9.67E-06	-0.2389	ORP150
33421_s_at301	AB016247	7.44E-05	2.58E-05	3.13E-05	-0.57287	SC5DL
38404_at302	M55153	7.44E-05	2.58E-05	4.77E-06	-0.27465	TGM2
553_g_at303	U02570	1.37E-05	2.81E-05	1.26E-06	0.432431	ARHGAP1
33903_at304	X04366	1.37E-05	2.81E-05	5.11E-06	0.346076	CAPN1
1499_at305	L10413	1.37E-05	2.81E-05	6.46E-06	0.207231	FNTA
39733_at306	AF055001	1.37E-05	2.81E-05	9.78E-06	-0.9457	HERPUD1
41502_at307	AI523538	1.37E-05	2.81E-05	0.004471	-0.1584	HIPK3
414_at308	X59373	1.37E-05	2.81E-05	1.31E-05	-0.22992	HOXD10
39343_at309	X99209	1.37E-05	2.81E-05	2.65E-05	0.239777	HRMT1L1
202_at310	M65217	1.37E-05	2.81E-05	1.02E-05	0.33377	HSF2
36985_at311	X17025	1.37E-05	2.81E-05	1.45E-05	-0.44351	IDI1
37319_at312	M35878	1.37E-05	2.81E-05	4.29E-05	-0.25267	IGFBP3

41728_at313	D63486	1.37E-05	2.81E-05	9.69E-06	0.235319	KIAA0152
37914_at314	AB002303	1.37E-05	2.81E-05	1.86E-05	-0.39642	KIAA0305
535_s_at315	U20816	1.37E-05	2.81E-05	4.92E-05	-0.20145	NFKB2
1269_at316	M61906	1.37E-05	2.81E-05	5.93E-06	-0.39875	PIK3R1
524_at317	U13695	1.37E-05	2.81E-05	1.31E-05	0.362255	PMS1
35850_f_at318	U38979	1.37E-05	2.81E-05	3.95E-05	0.158105	PMS2L9
382_at319	X70218	1.37E-05	2.81E-05	2.44E-06	-0.74691	PPP4C
39975_at320	AC002400	1.37E-05	2.81E-05	2.28E-06	-0.25834	
36336_s_at321	AC005390	1.37E-05	2.81E-05	2.99E-05	-0.24231	
34188_at322	AF070606	1.37E-05	2.81E-05	1.48E-06	-0.89337	
1842_at323	HG2724-HT2820	1.37E-05	2.81E-05	5.17E-06	-1.33814	
33334_at324	X84194	7.44E-05	4.67E-05	6.38E-05	0.23578	ACYP1
32607_at325	AF039656	0.00482	4.67E-05	0.000251	-0.73273	BASP1
37112_at326	AB002384	0.00482	4.67E-05	4.22E-05	0.548091	C6orf32
33774_at327	X98172	7.44E-05	4.67E-05	5.29E-07	0.507556	CASP8
486_at328	U60521	7.44E-05	4.67E-05	8.13E-06	-0.36762	CASP9
1924_at329	U11791	0.00482	4.67E-05	0.000363	-1.0232	CCNH
35695_at330	U67615	0.00482	4.67E-05	0.000948	1.23433	CHS1
41413_at331	AF037339	0.000344	4.67E-05	1.59E-05	-0.33549	CLPTM1
1789_at332	U65928	7.44E-05	4.67E-05	2.85E-07	0.408918	COPS5
41309_g_at333	U37408	7.44E-05	4.67E-05	3.06E-05	0.157458	CTBP1
37127_at334	AB023143	0.00482	4.67E-05	0.001982	0.215415	DEFCAP
41233_at335	AB014888	0.001377	4.67E-05	0.000204	-0.34841	DNAJB6
38037_at336	M60278	0.00482	4.67E-05	3.33E-05	-0.9007	DTR
40606_at337	U88629	0.000344	4.67E-05	9.58E-07	-0.32607	ELL2
1885_at338	M31899	0.000344	4.67E-05	0.000339	0.274507	ERCC3
39799_at339	M94856	7.44E-05	4.67E-05	4.99E-06	-0.23847	FABP5
36183_at340	X86779	0.001377	4.67E-05	1.08E-05	0.140032	FASTK
1772_s_at341	L00634	0.00482	4.67E-05	0.00019	0.205256	FNTA
39822_s_at342	AF078077	0.000344	4.67E-05	1.44E-05	-1.47649	GADD45B
717_at343	D87119	7.44E-05	4.67E-05	4.62E-06	0.557116	GS3955
33932_at344	X17644	7.44E-05	4.67E-05	6.72E-06	-0.71963	GSPT1
37393_at345	L19314	0.00482	4.67E-05	0.000922	-0.35113	HRY
1796_s_at346	U05681	7.44E-05	4.67E-05	3.37E-06	-0.35383	HSBCL3S2
1610_s_at347	J00139	0.00482	4.67E-05	0.000196	-0.12797	HUMFOL5
32640_at348	M24283	0.000344	4.67E-05	3.71E-06	-1.32611	ICAM1
1737_s_at349	M62403	7.44E-05	4.67E-05	5.57E-07	-0.53749	IGFBP4
1369_s_at350	M28130	7.44E-05	4.67E-05	8.02E-07	-2.27292	IL8
371_at351	Z56281	0.001377	4.67E-05	0.000243	0.309173	IRF3
2061_at352	L12002	7.44E-05	4.67E-05	1.23E-06	0.286717	ITGA4
32272_at353	K00558	0.001377	4.67E-05	0.002498	0.12909	K-ALPHA-1
34843_at354	AL044599	0.001377	4.67E-05	8.81E-05	0.321294	KIAA0222
41387_r_at355	AB002344	0.000344	4.67E-05	1.04E-05	-0.39307	KIAA0346
37363_at356	AB007889	7.44E-05	4.67E-05	2.33E-05	0.255643	KIAA0429
41243_at357	AB007916	0.00482	4.67E-05	0.000147	0.493018	KIAA0447

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3737b_at358	AB014538	0.000344	4.67E-05	1.98E-06	-0.63923	KIAA0638
3483l_at359	AF055004	7.44E-05	4.67E-05	9.29E-05	0.200537	KIAA0763
4067b_at360	AI148772	0.000344	4.67E-05	4.18E-06	-1.02619	KYNU
3516b_at361	AF064491	0.00482	4.67E-05	0.000148	-0.54215	LDB1
1846_at362	L78132	7.44E-05	4.67E-05	5.15E-07	0.358576	LGALS8
963_at363	X83441	7.44E-05	4.67E-05	6.75E-06	-0.17796	LIG4
3942s_at364	AF055581	7.44E-05	4.67E-05	5.69E-06	-1.05728	LNK
4045b_at365	AL049963	0.000344	4.67E-05	8.36E-07	-0.74421	LOC64116
3224b_g_at366	AF014837	0.00482	4.67E-05	0.000636	0.325349	M6A
1891_at367	D14497	0.001377	4.67E-05	3.68E-05	-0.58619	MAP3K8
1439_s_at368	X75346	7.44E-05	4.67E-05	1.99E-05	-0.37877	MAPKAPK2
3827s_at369	M62324	0.001377	4.67E-05	5.46E-05	-0.44552	MRF-1
4122b_at370	AB023208	0.000344	4.67E-05	1.37E-05	0.293901	MSF
3803b_at371	AF072928	0.001377	4.67E-05	1.13E-05	-0.3089	MTMR6
3869b_at372	AF045451	0.000344	4.67E-05	6.34E-06	-0.40149	NAB1
1378_g_at373	M58603	7.44E-05	4.67E-05	1.28E-06	-0.73537	NFKB1
519_g_at374	U07132	0.00482	4.67E-05	0.001821	-0.14679	NR1H2
3762s_at375	X75918	7.44E-05	4.67E-05	3.50E-05	-1.61126	NR4A2
547_s_at376	S77154	0.00482	4.67E-05	0.000304	-1.33785	NR4A2
3375b_at377	AB020657	0.00482	4.67E-05	2.75E-05	-0.50544	NS1-BP
1959_at378	D88674	7.44E-05	4.67E-05	6.26E-06	-0.99818	OAZIN
3994s_at379	U27459	0.00482	4.67E-05	3.39E-05	0.430016	ORC2L
358_at380	AF000545	7.44E-05	4.67E-05	3.48E-06	-0.85393	P2Y10
3827b_at381	AF005043	7.44E-05	4.67E-05	2.70E-06	0.408592	PARG
3836b_at382	AF026086	0.000344	4.67E-05	2.66E-06	0.297942	PEX1
3686l_at383	AJ001625	7.44E-05	4.67E-05	9.91E-05	0.36837	PEX3
3696s_at384	U30255	0.001377	4.67E-05	0.000826	0.325906	PGD
3537s_at385	M61906	0.000344	4.67E-05	0.000611	-0.2492	PIK3R1
3318l_at386	M60483	0.000344	4.67E-05	3.17E-05	-0.32565	PPP2CA
1241_at387	U14603	7.44E-05	4.67E-05	4.46E-05	0.427268	PTP4A2
4086b_at388	AF069517	0.001377	4.67E-05	0.000441	0.330897	RBM6
570_at389	M83221	0.000344	4.67E-05	1.58E-05	-0.26782	RELB
3829b_at390	AF037195	0.00482	4.67E-05	8.27E-05	0.959619	RGS14
1127_at391	L07597	0.00482	4.67E-05	0.000169	0.277243	RPS6KA1
1866_g_at392	X15217	7.44E-05	4.67E-05	3.77E-07	-0.2371	SKIL
3697b_at393	M20681	0.001377	4.67E-05	1.92E-05	-0.99917	SLC2A3
3654b_at394	AF030409	7.44E-05	4.67E-05	7.66E-06	0.412043	SLC9A6
3741b_at395	AJ224358	0.00482	4.67E-05	0.009613	0.14432	SURF5
3563l_at396	U49928	0.000344	4.67E-05	6.31E-06	0.352648	TAB1
3880b_at397	X89750	7.44E-05	4.67E-05	7.38E-06	-1.51687	TGIF
3283l_at398	AA453183	0.001377	4.67E-05	4.48E-05	-0.61646	TIM17
1372_at399	M31165	7.44E-05	4.67E-05	1.38E-06	-0.34617	TNFAIP6
3174b_at400	AF064090	0.001377	4.67E-05	4.05E-05	-0.38921	TNFSF14
3943b_at401	AF082557	0.001377	4.67E-05	2.23E-06	0.226994	TNKS
3883l_at402	D87448	0.00482	4.67E-05	0.000735	0.468196	TOPBP1
3386b_at403	X05276	0.00482	4.67E-05	8.97E-05	-0.50457	TPM4

33253_at404	D50919	0.00482	4.67E-05	4.02E-05	0.332326	TRIM14
1410_at405	J03258	0.00482	4.67E-05	8.78E-05	-0.33021	VDR
32383_at406	AB007973	0.00482	4.67E-05	0.000146	0.271053	
40873_f_at407	AF041081	0.00482	4.67E-05	5.92E-05	0.26539	
36250_at408	AI889718	7.44E-05	4.67E-05	0.000143	-0.15002	
37043_at409	AL021154	0.000344	4.67E-05	2.19E-06	-0.82935	
40711_at410	AL049340	0.000344	4.67E-05	4.87E-05	-0.91769	
39324_at411	AL050078	0.000344	4.67E-05	1.63E-05	-0.2875	
37442_at412	AL050378	0.000344	4.67E-05	5.72E-06	0.360577	
33683_at413	D50525	0.000344	4.67E-05	3.02E-06	0.486698	
31697_s_at414	J04755	7.44E-05	4.67E-05	6.75E-05	-0.37296	
40842_at415	M60784	7.44E-05	4.67E-05	1.24E-06	0.559903	
36101_s_at416	M63978	0.000344	4.67E-05	1.77E-06	-0.44762	
38093_at417	U90909	0.00482	4.67E-05	3.74E-05	-0.64272	
31526_f_at418	X63547	0.001377	4.67E-05	0.000303	0.505712	
32606_at419	AA135683	0.000344	5.23E-05	0.000289	-0.69258	BASP1
36209_at420	S78771	0.000344	5.23E-05	2.55E-06	-0.31389	BRD2
39411_at421	AL080156	0.000344	5.23E-05	3.52E-05	-0.94419	DKFZP434J214
1616_at422	D14838	0.000344	5.23E-05	7.34E-06	-0.50648	FGF9
35785_at423	W28281	0.000344	5.23E-05	8.96E-06	-1.09149	GABARAPL1
41386_i_at424	AB002344	7.44E-05	5.23E-05	8.48E-07	-1.00068	KIAA0346
37673_at425	U23070	0.000344	5.23E-05	3.62E-05	-0.12321	NMA
1069_at426	U04636	0.000344	5.23E-05	2.81E-06	-1.85123	PTGS2
471_f_at427	U47634	0.000344	5.23E-05	0.002405	-0.21686	TUBB4
1464_at428	S73149	0.000344	5.23E-05	0.003714	-0.15741	
36190_at429	M63256	0.000344	5.92E-05	6.54E-07	0.454561	CDR2
38003_s_at430	U94905	0.000344	5.92E-05	2.08E-05	0.388608	DGKZ
40843_at431	AF012023	7.44E-05	5.92E-05	1.02E-06	0.50623	ICAP-1A
1479_g_at432	L10717	0.000344	5.92E-05	0.000158	0.345558	ITK
38149_at433	D29642	0.000344	5.92E-05	8.30E-06	0.327019	KIAA0053
36279_at434	AB011128	0.000344	5.92E-05	0.000584	0.151161	KIAA0556
39777_at435	AF075587	0.000344	5.92E-05	7.55E-06	0.4405	KIAA0916
138_at436	U66464	0.000344	5.92E-05	2.93E-05	0.255675	MAP4K1
36127_g_at437	U18919	0.000344	5.92E-05	0.000573	0.277847	NBP
1980_s_at438	X58965	0.000344	5.92E-05	7.34E-05	0.231912	NME2
40896_at439	X13403	7.44E-05	5.92E-05	4.21E-07	0.146032	POU2F1
32075_at440	D89859	0.000344	5.92E-05	1.56E-05	0.375402	ZFP161
36813_at441	AF052100	0.000344	5.92E-05	1.37E-05	0.290021	
39693_at442	N53547	7.44E-05	7.24E-05	1.80E-07	0.296678	MGC5508
33909_at443	L35013	0.000344	7.24E-05	0.000112	-0.17331	SF3B4
41010_at444	Y17829	7.44E-05	7.24E-05	5.49E-06	-0.6508	SYN47
40552_s_at445	AL049987	7.44E-05	7.24E-05	2.39E-05	0.193082	
37904_s_at446	X66436	0.000344	7.24E-05	1.88E-06	-0.26662	
39403_at447	Z80345	7.44E-05	9.64E-05	7.31E-06	0.412137	ACADS
2002_s_at448	U27467	7.44E-05	9.64E-05	5.65E-06	-0.56637	BCL2A1
34484_at449	AI961669	7.44E-05	9.64E-05	0.000107	-0.1656	BIG2

37294_at450	X61123	7.44E-05	9.64E-05	4.17E-07	-1.15256	BTG1
32973_g_at451	U49187	7.44E-05	9.64E-05	3.53E-06	0.511392	C6orf32
36650_at452	D13639	7.44E-05	9.64E-05	8.56E-06	-0.64255	CCND2
34845_at453	AL035398	7.44E-05	9.64E-05	0.000153	0.353395	CGI-51
529_at454	U15932	7.44E-05	9.64E-05	0.00031	-1.26603	DUSP5
38599_s_at455	AD001530	7.44E-05	9.64E-05	3.06E-05	-0.37019	DXS9928E
37762_at456	Y07909	7.44E-05	9.64E-05	0.000161	-0.23489	EMP1
38226_at457	W27152	7.44E-05	9.64E-05	0.000502	0.186359	FLJ10569
39704_s_at458	L17131	7.44E-05	9.64E-05	1.48E-05	-0.24039	HMGIY
38299_at459	X04430	7.44E-05	9.64E-05	4.15E-05	-0.21816	IL6
41614_at460	AB014608	7.44E-05	9.64E-05	4.59E-06	0.41494	KIAA0708
40060_r_at461	AF061258	7.44E-05	9.64E-05	1.58E-06	0.622201	LIM
35833_at462	U90919	7.44E-05	9.64E-05	7.23E-06	-0.50014	LOC57862
40390_at463	J05037	7.44E-05	9.64E-05	0.000185	-0.19243	SDS
40638_at464	X70944	7.44E-05	9.64E-05	2.08E-05	-0.72892	SFPQ
32165_at465	L41887	7.44E-05	9.64E-05	6.74E-06	-0.52203	SFRS7
32649_at466	X59871	7.44E-05	9.64E-05	1.91E-05	0.376648	TCF7
38801_at467	AI742846	7.44E-05	9.64E-05	0.000374	-0.48069	VAPA
1743_s_at468	HG2007-HT2056	7.44E-05	9.64E-05	4.01E-06	-0.41408	
32145_at469	X58141	7.44E-05	9.64E-05	1.75E-06	0.384254	
34979_at470	AB018323	7.44E-05	0.000106	2.41E-05	0.432301	GASC1
33916_at471	AB023192	7.44E-05	0.000106	0.000138	0.196185	I-1
41372_at472	AB020638	7.44E-05	0.000106	5.26E-05	0.233629	KIAA0831
40396_at473	U49395	7.44E-05	0.000106	0.001916	0.169175	P2RX5
36935_at474	M23379	7.44E-05	0.000106	3.22E-05	0.42571	RASA1
32213_at475	AF034176	7.44E-05	0.000106	0.000333	0.332105	
34677_f_at476	AJ012755	7.44E-05	0.000106	0.000296	0.26445	
38704_at477	AB007934	7.44E-05	0.000119	6.08E-06	0.345799	ACF7
37027_at478	M80899	7.44E-05	0.000119	2.48E-05	0.419409	AHNAK
34657_at479	AB014529	7.44E-05	0.000119	1.84E-05	0.43403	AKAP11
36573_at480	U37547	7.44E-05	0.000119	6.74E-06	-0.71736	BIRC2
36634_at481	U72649	7.44E-05	0.000119	0.000207	-0.30079	BTG2
34333_at482	D49738	7.44E-05	0.000119	0.000136	0.292742	CKAP1
37453_at483	AJ006267	7.44E-05	0.000119	7.19E-06	0.427023	CLPX
34404_at484	W28167	7.44E-05	0.000119	1.16E-05	0.214921	COPS7A
1243_at485	U18300	7.44E-05	0.000119	2.43E-06	0.183171	DDB2
35682_at486	AI133727	7.44E-05	0.000119	1.43E-06	0.181464	FLB6421
36647_at487	AA526812	7.44E-05	0.000119	0.000106	0.259476	FLJ10326
318_at488	D64142	7.44E-05	0.000119	1.66E-05	0.528036	H1FX
38913_at489	U60319	7.44E-05	0.000119	0.001064	0.194324	HFE
35372_r_at490	M17017	7.44E-05	0.000119	1.43E-06	-1.74073	IL8
34336_at491	D32053	7.44E-05	0.000119	0.003279	0.222661	KARS
35374_at492	AB007914	7.44E-05	0.000119	7.13E-05	0.302838	KIAA0445
35974_at493	U10485	7.44E-05	0.000119	7.40E-06	0.270352	LRMP
198_s_at494	U29656	7.44E-05	0.000119	4.31E-06	0.471876	NME3

33755_at495	AB014604	7.44E-05	0.000119	1.72E-05	0.425787	OSBPL3
835_at496	U41745	7.44E-05	0.000119	0.00204	0.230274	PDAP1
858_at497	S90469	7.44E-05	0.000119	5.56E-06	-0.2636	POR
875_g_at498	M26683	7.44E-05	0.000119	3.70E-06	-0.16179	SCYA2
37379_at499	X81789	7.44E-05	0.000119	2.23E-05	0.143079	SF3A3
41127_at500	L14595	7.44E-05	0.000119	3.55E-05	-0.1953	SLC1A4
38341_at501	AL079286	7.44E-05	0.000119	0.000245	0.165851	STAU2
37343_s_at502	AA845349	7.44E-05	0.000119	7.78E-07	0.457176	TRIP7
40414_at503	X59303	7.44E-05	0.000119	0.000124	0.224891	VARS2
41366_at504	AB023219	7.44E-05	0.000119	1.41E-05	0.316475	
38433_at505	M58603	7.44E-05	0.000129	9.08E-06	-0.56835	NFKB1
32741_at506	X77723	7.44E-05	0.000129	0.006788	-0.24317	RAB5EP
41384_at507	AF117829	7.44E-05	0.000129	2.61E-06	-0.57516	RIPK2
34357_g_at508	U52960	7.44E-05	0.000129	0.001042	-0.24648	SURB7
38253_at509	U84011	0.00482	0.000149	0.000134	0.286331	AGL
32629_f_at510	U90552	0.000344	0.000149	0.000182	0.288509	BTN3A1
40733_at511	M16336	0.00482	0.000149	0.000224	0.218007	CD2
2031_s_at512	U03106	0.000344	0.000149	0.000252	-0.87784	CDKN1A
38664_at513	AB009285	0.001377	0.000149	0.000137	0.235726	CFDP1
34683_at514	U63289	0.001377	0.000149	0.001722	-0.43517	CUGBP1
357_at515	AF000430	0.00482	0.000149	0.000694	-0.19887	DNM1L
1292_at516	L11329	0.001377	0.000149	0.000142	-0.56584	DUSP2
38283_at517	AB007619	0.00482	0.000149	0.002073	0.198391	EBAG9
37313_at518	X81625	0.00482	0.000149	6.92E-05	-0.80689	ETF1
38313_at519	AL050128	0.000344	0.000149	1.81E-05	0.459416	FAM8A1
36669_at520	L49169	0.001377	0.000149	8.18E-05	-2.09549	FOSB
37903_at521	L25665	0.000344	0.000149	3.34E-06	-0.4513	GNL1
32591_at522	AI494623	0.00482	0.000149	0.000304	0.187206	HCDI
40576_f_at523	D89678	0.001377	0.000149	3.03E-05	0.197298	HNRPDL
1635_at524	U07563	0.000344	0.000149	1.02E-05	-0.23627	HSABLGR3
40913_at525	W28589	0.00482	0.000149	0.000129	0.170457	HSPD1
41253_at526	N29665	0.000344	0.000149	3.34E-05	0.593294	KIAA0618
41447_at527	AB023207	0.000344	0.000149	8.64E-06	-0.4056	KIAA0990
41710_at528	AL079277	0.00482	0.000149	0.000161	0.200656	LOC54103
34770_at529	Z14138	0.001377	0.000149	0.000197	-0.85008	MAP3K8
35969_at530	N23137	0.001377	0.000149	4.12E-06	0.244083	MPHOSPH9
32733_at531	AF050640	0.001377	0.000149	6.03E-05	0.324021	NDUFS2
39735_at532	AF069987	0.001377	0.000149	4.44E-05	0.203382	NIT1
41656_at533	AF043325	0.000344	0.000149	1.06E-05	0.328186	NMT2
1102_s_at534	M10901	0.001377	0.000149	1.91E-05	-0.58982	NR3C1
36636_at535	M12267	0.000344	0.000149	4.07E-06	-0.3279	OAT
38526_at536	U02882	0.00482	0.000149	0.000223	-0.99878	PDE4D
34998_at537	AF059531	0.000344	0.000149	6.73E-06	0.546441	PRMT3
39253_s_at538	M29893	0.001377	0.000149	9.96E-05	-0.15688	RALA
33457_at539	AB029028	0.001377	0.000149	9.11E-06	0.482258	RAP140
40391_at540	AB007448	0.00482	0.000149	0.000777	-0.319	SLC22A4

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3789_at541	D87969	0.00482	0.000149	0.001578	0.401991	SLC35A1
4081_at542	U66615	0.00482	0.000149	0.000196	0.235993	SMARCC1
4165_at543	U46691	0.00482	0.000149	1.48E-05	-0.85179	SUPT6H
4084_at544	AF049910	0.00482	0.000149	0.000373	-0.32787	TACC1
115_at545	X14787	0.001377	0.000149	2.88E-05	-0.19161	THBS1
4014_at546	AI375913	0.00482	0.000149	0.000905	-0.12102	TOP2A
3367_f_at547	X02344	0.001377	0.000149	0.00414	-0.20405	TUBB2
3766_at548	AF104421	0.000344	0.000149	6.50E-06	0.349373	UROD
1388_g_at549	J03258	0.000344	0.000149	1.21E-06	-0.58295	VDR
4056_at550	M58297	0.000344	0.000149	1.57E-05	0.185829	ZNF42
3321_g_at551	Y11681	0.000344	0.000149	1.92E-05	0.234481	
4142_at552	AF104942	0.001377	0.00019	4.83E-05	0.464438	ABCC5
3214_s_at553	L07261	0.000344	0.00019	0.003564	0.29763	ADD1
287_at554	L19871	0.001377	0.00019	0.000105	-0.19867	ATF3
3766_at555	J04027	0.000344	0.00019	0.000133	-0.42466	ATP2B1
4108_at556	M83363	0.001377	0.00019	0.004471	0.177565	ATP2B4
3184_at557	AF038195	0.000344	0.00019	0.000134	0.281425	BCS1L
3621_g_at558	S78771	0.001377	0.00019	0.000145	-0.24109	BRD2
650_s_at559	L07044	0.001377	0.00019	0.000284	0.186013	CAMK2G
1116_at560	M28170	0.000344	0.00019	2.96E-05	0.356602	CD19
3522_at561	Y08682	0.000344	0.00019	0.000118	0.17398	CPT1B
3750_at562	AF046059	0.001377	0.00019	0.000665	0.204072	CREME9
649_s_at563	L06797	0.001377	0.00019	0.000455	-0.93505	CXCR4
631_g_at564	L39874	0.000344	0.00019	0.000354	0.353702	DCTD
3183_at565	AC004475	0.000344	0.00019	2.86E-05	0.25205	DKFZP434E2216
3826_at566	AI538172	0.001377	0.00019	0.000621	0.243057	DKFZp761B2423
3736_at567	AF010187	0.000344	0.00019	1.00E-05	0.361895	FIBP
3319_g_at568	AW051579	0.000344	0.00019	0.000258	0.390285	FLJ10512
4076_at569	M22632	0.001377	0.00019	1.34E-05	0.157239	GOT2
413_at570	X59372	0.001377	0.00019	0.000528	-0.12959	HOXD9
4108_at571	X12433	0.000344	0.00019	1.07E-05	-0.39946	HS1-2
3231_s_at572	X15183	0.000344	0.00019	0.000645	-0.22973	HSPCA
3935_at573	AI912041	0.001377	0.00019	5.21E-05	-0.38517	HSPE1
3866_at574	X75315	0.000344	0.00019	0.010841	-0.64335	HSRNASEB
253_g_at575	L42324	0.000344	0.00019	0.000262	-0.31758	HUMFRCG
3233_at576	X69433	0.001377	0.00019	0.002925	0.209735	IDH2
3670_at577	Y00093	0.000344	0.00019	2.60E-05	-0.39318	ITGAX
3908_at578	M88458	0.001377	0.00019	0.002031	-0.15998	KDELR2
3654_s_at579	AB011114	0.000344	0.00019	3.13E-05	0.278271	KIAA0542
3891_at580	AB011135	0.000344	0.00019	0.000149	0.247752	KIAA0563
4067_at581	U57721	0.001377	0.00019	3.47E-05	-0.23188	KYNU
3944_at582	Y11395	0.001377	0.00019	8.58E-05	0.34059	LANCL1
4159_at583	AI652660	0.000344	0.00019	2.28E-05	0.385107	LOC51112
3235_at584	AB026118	0.001377	0.00019	4.47E-06	-0.24886	MALT1
4046_at585	AB011144	0.000344	0.00019	9.36E-05	0.26851	MCM3AP
4169_at586	AI620381	0.000344	0.00019	8.06E-06	0.29605	MGC3077

38655_at587	AI525633	0.000344	0.00019	2.44E-05	0.170916	MGC5576
40074_at588	X16396	0.000344	0.00019	3.27E-06	-0.6151	MTHFD2
37724_at589	V00568	0.000344	0.00019	0.000769	0.549224	MYC
31896_at590	AL050281	0.000344	0.00019	2.85E-06	0.30517	NAG
40686_at591	AI985272	0.000344	0.00019	0.000474	-0.2571	NMB
31794_at592	D38524	0.000344	0.00019	0.001313	0.228851	NT5B
34491_at593	AJ225089	0.000344	0.00019	0.000531	-0.2589	OASL
36413_at594	Z82200	0.000344	0.00019	0.000136	-0.28579	P2Y10
40791_at595	X63564	0.001377	0.00019	1.70E-05	-0.28202	POLR2A
32157_at596	S57501	0.001377	0.00019	0.002179	0.267744	PPP1CA
1217_g_at597	X07109	0.000344	0.00019	0.000694	0.167774	PRKCB1
1074_at598	M28209	0.000344	0.00019	0.000392	-0.52456	RAB1
1055_g_at599	M87339	0.000344	0.00019	3.41E-05	0.248151	RFC4
35685_at600	Z14000	0.000344	0.00019	3.91E-06	-0.33734	RING1
40875_s_at601	X06815	0.000344	0.00019	3.50E-05	0.293968	SNRP70
37757_at602	L23959	0.000344	0.00019	1.82E-05	-0.36834	TFDP1
32853_at603	AB018262	0.000344	0.00019	0.000241	0.319056	TOMM70A
32793_at604	X00437	0.001377	0.00019	0.00022	0.248344	TRB@
35214_at605	AF061016	0.000344	0.00019	0.000264	0.349913	UGDH
38337_at606	U62392	0.000344	0.00019	2.74E-05	-0.65983	ZNF193
34544_at607	X78925	0.001377	0.00019	0.001253	-0.28003	ZNF267
39932_at608	AI655015	0.001377	0.00019	0.00444	0.74681	
32672_at609	AL049387	0.001377	0.00019	5.12E-06	0.379296	
41219_at610	AL050376	0.000344	0.00019	0.00026	0.410405	
34435_at611	AB008775	0.000344	0.000304	1.88E-06	-0.80745	AQP9
40175_at612	AI141670	0.000344	0.000304	1.60E-06	-0.2494	CLCN2
35715_at613	AL080071	0.000344	0.000304	3.12E-06	0.237367	DKFZP564M082
35163_at614	AB028964	0.000344	0.000304	5.07E-05	0.351352	KIAA1041
33249_at615	M16801	0.001377	0.000304	0.000458	0.412733	NR3C2
39131_at616	N36842	0.001377	0.000304	0.000577	0.172944	UPF3A
33413_at617	AL096752	0.000344	0.000304	0.000323	-0.20419	
38743_at618	U76421	0.000344	0.000402	0.000278	0.226301	ADARB1
40745_at619	L13939	0.001377	0.000402	0.000215	0.180874	AP1B1
39347_at620	X97074	0.001377	0.000402	0.001924	0.298218	AP2S1
818_s_at621	U72936	0.000344	0.000402	1.03E-05	0.356824	ATRX
36945_at622	X94910	0.000344	0.000402	0.000204	0.249294	C12orf8
40404_s_at623	U18291	0.000344	0.000402	2.45E-05	0.594377	CDC16
1273_r_at624	L22005	0.001377	0.000402	0.000111	-0.15257	CDC34
32833_at625	M59287	0.00482	0.000402	0.000276	-0.72279	CLK1
35319_at626	U25435	0.000344	0.000402	0.000648	0.264876	CTCF
630_at627	L39874	0.000344	0.000402	2.41E-05	0.211923	DCTD
34647_at628	X52104	0.000344	0.000402	0.000159	0.317963	DDX5
33776_at629	AL050062	0.000344	0.000402	0.000377	0.36401	DKFZP566K023
35799_at630	AL080081	0.00482	0.000402	0.000103	-0.60871	DNAJB9
40375_at631	X63741	0.001377	0.000402	0.000175	-0.59207	EGR3
777_at632	D13988	0.001377	0.000402	0.000371	0.14676	GDI2

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1368_at633	M27492	0.000344	0.000402	2.01E-06	-0.32619	IL1R1
3341_g_at634	S66213	0.000344	0.000402	9.56E-05	0.247863	ITGA6
3431_at635	AJ005896	0.000344	0.000402	5.38E-05	0.210462	JM4
3547_at636	Y10745	0.00482	0.000402	6.39E-05	-0.30524	KCNJ15
3483_at637	AB002374	0.00482	0.000402	0.000916	0.20284	KIAA0376
4169_at638	AB007874	0.001377	0.000402	0.000181	-0.21662	KIAA0414
3322_at639	AB011133	0.00482	0.000402	0.000521	0.302843	KIAA0561
3933_at640	AB018335	0.00482	0.000402	9.03E-05	0.234274	KIAA0792
3737_i_at641	M13452	0.00482	0.000402	0.00148	-0.28339	LMNA
3257_at642	X68836	0.00482	0.000402	2.15E-05	-0.57967	MAT2A
3757_at643	U79256	0.000344	0.000402	2.24E-05	0.328028	MGC14258
3718_at644	X76538	0.001377	0.000402	5.62E-05	0.408464	MPV17
3653_at645	AB011093	0.000344	0.000402	0.000101	0.612928	P114-RHO-GEF
1224_at646	X66363	0.001377	0.000402	6.80E-05	-0.24041	PCTK1
4146_at647	U13695	0.00482	0.000402	2.31E-05	0.31531	PMS1
3535_at648	D87078	0.000344	0.000402	3.88E-05	0.497225	PUM2
109_at649	Z97074	0.001377	0.000402	3.97E-05	0.296662	RAB9P40
3998_at650	X90530	0.000344	0.000402	3.52E-05	0.254197	RAGB
3691_at651	U75679	0.001377	0.000402	0.000139	-0.29594	SLBP
3876_at652	AF007142	0.000344	0.000402	3.15E-06	0.678734	
3671_at653	AL021977	0.00482	0.000402	8.82E-05	-0.82538	
3863_at654	AL080192	0.001377	0.000402	4.26E-05	0.201319	
956_at655	HG1980-HT2023	0.00482	0.000402	0.003775	-0.48359	
3400_at656	U47924	0.001377	0.000402	0.000134	0.52195	
1933_g_at657	U83661	0.000344	0.000444	9.97E-06	0.270218	ABCC5
3970_at658	AI961929	0.000344	0.000444	1.88E-05	0.461528	ARHGAP1
3964_at659	X78817	0.000344	0.000444	2.82E-05	0.281835	ARHGAP4
3440_at660	AL080164	0.000344	0.000444	0.000218	0.268161	DKFZP564C1940
3721_at661	X90392	0.000344	0.000444	0.000208	0.150242	DNASE1L1
4085_at662	AI561196	0.000344	0.000444	0.000156	0.302434	FLJ11806
3710_at663	AJ008112	0.000344	0.000444	0.000246	-0.32126	FMNL
3801_at664	M94630	0.000344	0.000444	0.000244	0.274532	HNRPD
3572_at665	M38180	0.000344	0.000444	0.003037	-0.15741	HSD3B1
3183_at666	U79274	0.000344	0.000444	9.67E-05	0.285563	HSU79274
4022_s_at667	AB014585	0.000344	0.000444	6.48E-05	0.460196	KIAA0685
3468_at668	AB029001	0.000344	0.000444	0.000183	-0.33324	KIAA1078
3273_at669	AA045160	0.000344	0.000444	4.62E-05	0.179556	MRPS14
4081_at670	M96824	0.000344	0.000444	2.18E-05	0.139326	NUCB1
381_s_at671	Y10055	0.000344	0.000444	9.91E-06	0.176067	PIK3CD
3802_s_at672	Z54367	0.000344	0.000444	1.30E-05	-0.39738	PLEC1
3479_at673	AF014402	0.000344	0.000444	7.63E-05	0.147061	PPAP2A
4051_at674	M30773	0.000344	0.000444	0.001161	0.41229	PPP3R1
878_s_at675	M29386	0.000344	0.000444	6.26E-05	-0.23554	PRL
1852_at676	X02910	0.000344	0.000444	0.001378	-0.17579	TNF
3491_s_at677	S76792	0.000344	0.000444	0.000211	-0.16737	TNFRSF4

37685_s_at678	Y09008	0.000344	0.000444	0.000352	0.168444	UNG
40147_at679	U18009	0.000344	0.000444	0.002896	0.204706	VATI
1307_at680	D14533	0.000344	0.000444	0.000837	0.246085	XPA
36564_at681	W27419	0.000344	0.000444	2.83E-05	-0.44121	
35001_at682	Z85986	0.000344	0.000444	0.000407	-0.2149	
36607_at683	Z99716	0.000344	0.000444	5.14E-05	0.324642	
35364_at684	U50939	0.001377	0.000525	1.19E-05	0.235552	APPBP1
36554_at685	Y15521	0.00482	0.000525	0.000492	-0.28889	ASMTL
37948_at686	J05682	0.00482	0.000525	0.000291	-0.33004	ATP6C
37947_at687	D26362	0.00482	0.000525	0.000707	0.247252	BRD3
39525_at688	AL120687	0.001377	0.000525	1.21E-05	-0.55731	CSH1
40646_at689	U20350	0.00482	0.000525	0.010386	0.383475	CX3CR1
37975_at690	X04011	0.00482	0.000525	0.000154	0.348439	CYBB
36573_at691	U78524	0.001377	0.000525	6.56E-05	-0.36872	DDXBP1
39182_at692	U87947	0.001377	0.000525	5.05E-05	-0.29673	EMP3
39876_at693	AL035252	0.00482	0.000525	0.003735	0.074075	ENTPD6
37307_at694	X04828	0.00482	0.000525	0.0015	0.256297	GNAI2
32321_at695	X56841	0.001377	0.000525	4.37E-05	0.338907	HLA-E
1185_at696	D49410	0.00482	0.000525	0.00016	-0.21753	HUMIL3RA12
40815_g_at697	L40586	0.00482	0.000525	3.02E-05	-0.20891	IDS
37603_at698	X52015	0.00482	0.000525	0.00032	-0.54051	IL1RN
37651_at699	D31888	0.00482	0.000525	7.50E-06	-0.44687	KIAA0071
38394_at700	D42047	0.001377	0.000525	3.50E-05	0.226884	KIAA0089
35442_at701	AB007958	0.00482	0.000525	0.00023	0.259725	KIAA0489
35252_at702	AB011100	0.00482	0.000525	0.000193	0.418151	KIAA0528
31803_at703	AB014553	0.00482	0.000525	0.002002	-0.25439	KIAA0653
37308_at704	AI888084	0.001377	0.000525	3.57E-05	0.391754	KIAA1624
32184_at705	X61118	0.00482	0.000525	0.001631	0.292879	LMO2
34874_at706	AJ004832	0.00482	0.000525	0.001715	0.30393	NTE
41665_at707	AB020631	0.001377	0.000525	0.000212	0.379354	PCF11
37143_s_at708	AB002359	0.00482	0.000525	2.36E-05	0.271468	PFAS
37111_g_at709	AB012229	0.001377	0.000525	0.000168	-0.59579	PFKFB3
32210_at710	M83088	0.001377	0.000525	3.50E-05	0.439367	PGM1
37392_at711	X84908	0.001377	0.000525	2.25E-05	0.331887	PHKB
40624_at712	U48250	0.001377	0.000525	8.51E-05	-0.2234	PRKCBP2
41853_at713	AB007851	0.000344	0.000525	1.95E-05	0.481768	PRPSAP2
32070_at714	X97267	0.00482	0.000525	0.000303	0.211707	PTPRCAP
32737_at715	M64595	0.00482	0.000525	0.004436	0.170959	RAC2
36575_at716	S59049	0.001377	0.000525	0.000915	-0.61362	RGS1
34714_at717	AL050267	0.00482	0.000525	0.000204	0.311003	SAMHD1
41451_s_at718	W28498	0.00482	0.000525	1.70E-05	-0.57386	SAR1
41199_s_at719	W27050	0.00482	0.000525	2.37E-05	-0.587	SFPQ
37273_at720	X92762	0.00482	0.000525	0.000116	0.283179	TAZ
34741_at721	U18422	0.001377	0.000525	0.000279	-0.14486	TFDP2
950_at722	D87127	0.001377	0.000525	0.000126	-0.32216	TLOC1
1468_at723	U12595	0.001377	0.000525	1.07E-05	0.347309	TRAP1

40065_at~~724~~	AF046024	0.00482	0.000525	0.000469	0.405378	UBE1C
32235_at~~725~~	AF032456	0.001377	0.000525	5.89E-05	0.269833	UBE2G2
41532_at~~726~~	Y09723	0.00482	0.000525	0.000854	-0.23772	ZNF151
33297_at~~727~~	AL031778	0.00482	0.000525	0.000239	0.178561	
36212_at~~728~~	AL049218	0.00482	0.000525	0.001951	0.238837	
35187_at~~729~~	AL080216	0.00482	0.000525	0.000349	0.311531	
32855_at~~730~~	L00352	0.00482	0.000525	0.005084	-0.39882	
856_at~~731~~	S79267	0.00482	0.000525	0.000908	-0.19945	
31615_i_at~~732~~	U94902	0.00482	0.000525	0.002556	-0.17833	
33198_at~~733~~	AA206524	0.000344	0.000567	0.000172	0.161868	BART1
37347_at~~734~~	AA926959	0.000344	0.000567	8.47E-05	0.169915	CKS1
876_at~~735~~	M27543	0.000344	0.000567	0.000319	-0.48924	GNAI3
41555_s_at~~736~~	AF019386	0.000344	0.000567	0.000399	-0.18103	HS3ST1
38545_at~~737~~	AB006537	0.000344	0.000567	0.000658	-0.1547	IL1RAP
38145_at~~738~~	AJ001306	0.000344	0.000567	5.70E-05	0.338818	INADL
32235_at~~739~~	AB011116	0.000344	0.000567	0.000355	0.25593	KIAA0544
33924_at~~740~~	AB029014	0.000344	0.000567	0.001352	-0.1261	KIAA1091
34839_at~~741~~	AB029027	0.000344	0.000567	0.00209	0.180974	KIAA1104
36690_at~~742~~	M10901	0.000344	0.000567	4.00E-05	-0.42455	NR3C1
352_at~~743~~	D30036	0.000344	0.000567	5.62E-05	-0.15539	PITPN
40129_at~~744~~	U47077	0.000344	0.000567	0.001173	0.30799	PRKDC
33212_at~~745~~	AF006751	0.000344	0.000567	3.40E-05	-0.23462	RRBP1
33706_at~~746~~	AB006198	0.000344	0.000567	0.001465	0.256734	SART1
40104_at~~747~~	D63780	0.000344	0.000567	0.00021	0.374406	STK25
33850_at~~748~~	W28892	0.000344	0.000567	8.26E-05	0.803602	SUI1
890_at~~749~~	M74524	0.000344	0.000567	0.000421	-0.31531	UBE2A
41790_at~~750~~	AL031230	0.000344	0.000567	6.83E-05	0.272378	
37308_at~~751~~	AF057160	0.001377	0.000588	0.000279	0.307281	ADPRTL1
39336_at~~752~~	M74491	0.001377	0.000588	3.02E-05	0.170825	ARF3
36872_at~~753~~	AL120559	0.001377	0.000588	4.80E-05	-0.64478	ARPP-19
40108_at~~754~~	D13630	0.001377	0.000588	3.01E-05	-0.42457	BZAP45
40452_at~~755~~	U83246	0.001377	0.000588	0.003502	0.133045	CPNE1
31852_at~~756~~	AL050390	0.001377	0.000588	0.000139	0.231898	DKFZP564O043
36201_at~~757~~	D13315	0.001377	0.000588	0.000203	0.371377	GLO1
2090_i_at~~758~~	H12458	0.001377	0.000588	5.42E-05	-0.22578	H12458 yj12d03.s1
35738_at~~759~~	AI347088	0.001377	0.000588	0.000151	0.321012	HMG17L3
998_s_at~~760~~	X59770	0.001377	0.000588	0.001417	-0.36292	IL1R2
40461_at~~761~~	AB007855	0.000344	0.000588	1.02E-05	0.086396	KIAA0395
36213_at~~762~~	AB016816	0.001377	0.000588	0.000751	0.146218	MASL1
518_at~~763~~	U07132	0.001377	0.000588	0.002035	-0.27336	NR1H2
35835_at~~764~~	AB019409	0.001377	0.000588	0.001479	0.154377	PDL-108
36502_at~~765~~	AB020641	0.001377	0.000588	0.00342	0.174568	PFTK1
40521_at~~766~~	AL050259	0.001377	0.000588	0.001864	0.272972	RAB2L
35235_g_at~~767~~	AA099265	0.001377	0.000588	0.000614	0.38275	RECK
1856_at~~768~~	X75042	0.001377	0.000588	6.85E-05	-0.39572	REL

34304_s_at769	AL050290	0.001377	0.000588	0.002426	-0.28771	SAT
39390_at770	AJ006417	0.001377	0.000588	0.000125	-0.18595	TBCD
41445_at771	X02812	0.001377	0.000588	1.78E-05	-0.16423	TGFB1
36243_at772	AL050262	0.001377	0.000588	0.0031	0.348226	TLR1
33615_at773	X16576	0.001377	0.000588	9.49E-05	0.431692	ZNF46
41362_at774	X91249	0.000344	0.000609	1.04E-05	-0.3925	ABCG1
34310_at775	Y00486	0.000344	0.000609	0.000297	0.259418	APRT
32772_s_at776	U10473	0.000344	0.000609	0.000103	-0.15424	B4GALT1
40141_at777	AB014595	0.000344	0.000609	5.19E-05	0.320955	CUL4B
33791_at778	Y15227	0.000344	0.000609	4.08E-05	0.222481	DLEU1
32163_s_at779	U85267	0.000344	0.000609	0.000131	0.142894	DSCR1
35295_at780	AB019036	0.000344	0.000609	0.000336	0.177649	GGPS1
824_at781	U90313	0.000344	0.000609	0.001838	-0.25377	GSTTLp28
1589_s_at782	L42243	0.000344	0.000609	0.000201	0.403838	HUMIFNAM08
35731_at783	X16983	0.000344	0.000609	0.000317	0.232935	ITGA4
35830_at784	AB002368	0.000344	0.000609	0.001709	0.215217	KIAA0370
36171_at785	AI521453	0.000344	0.000609	0.000707	-0.22735	PC4
32140_at786	Y08110	0.000344	0.000609	9.87E-05	0.260436	SORL1
1858_at787	D38122	0.000344	0.000609	6.27E-05	-0.61781	TNFSF6
36950_at788	U49278	0.000344	0.000609	0.000173	0.204424	UBE2V1
39420_at789	X99050	0.000344	0.000609	7.72E-05	0.289751	UVRAG
39756_g_at790	Z93930	0.000344	0.000609	0.00015	-0.26558	XBP1
38053_s_at791	AF015767	0.000344	0.000659	0.000199	0.578977	BRE
37907_at792	M34677	0.000344	0.000659	0.000647	0.198622	F8A
1666_at793	J00210	0.000344	0.000659	0.002453	-0.18828	IFNA1
41345_at794	AJ007583	0.000344	0.000659	0.00506	-0.12644	LARGE
2059_s_at795	M36881	0.000344	0.000659	0.000302	0.328248	LCK
36174_at796	X70326	0.000344	0.000659	0.000132	-0.58974	MACMARCKS
32225_at797	M64571	0.000344	0.000659	0.000158	0.157573	MAP4
38605_at798	AI345944	0.000344	0.000659	0.000363	0.311507	NDUFB1
1695_at799	D23662	0.000344	0.000659	0.000171	0.289452	NEDD8
38590_r_at800	M14630	0.000344	0.000659	1.26E-05	-0.1626	PTMA
41763_g_at801	D64015	0.000344	0.000659	0.001012	0.195679	TIAL1
32323_at802	M63582	0.000344	0.000659	2.66E-05	-0.39175	
35564_at803	U79300	0.000344	0.000659	0.000196	-0.16218	
40960_at804	D29805	0.00482	0.000812	0.000289	-0.23044	B4GALT1
1913_at805	U47414	0.001377	0.000812	0.000137	0.262974	CCNG2
266_s_at806	L33930	0.001377	0.000812	5.56E-06	0.343203	CD24
32111_at807	AL050164	0.00482	0.000812	0.000345	0.307729	CDYL
40082_at808	D10040	0.001377	0.000812	1.49E-05	-0.45708	FACL2
37187_at809	M36820	0.00482	0.000812	7.67E-05	-0.49075	GRO2
466_at810	U77948	0.00482	0.000812	0.000511	0.286776	GTF2I
41484_r_at811	X56681	0.00482	0.000812	0.000503	-0.18359	JUND
35224_at812	AF070569	0.00482	0.000812	0.000446	-0.6104	MGC14376
34253_at813	W28205	0.00482	0.000812	0.00017	-0.21741	MKLN1
1719_at814	U61981	0.001377	0.000812	0.000725	0.203996	MSH3

39707_at815	AB014547	0.001377	0.000812	7.73E-05	0.217806	MTMR4
39507_at816	AL050366	0.00482	0.000812	0.001126	0.421541	OGT
35714_at817	U89606	0.001377	0.000812	6.13E-05	-0.19512	PDXK
1810_s_at818	D10495	0.00482	0.000812	0.000433	0.290156	PRKCD
32783_at819	D42063	0.001377	0.000812	0.000346	-0.52828	RANBP2
41446_f_at820	H68340	0.00482	0.000812	0.004081	-0.3419	RNAHP
41544_at821	AF059617	0.001377	0.000812	0.00012	-0.27807	SNK
32166_at822	AB028950	0.00482	0.000812	0.000365	0.313606	TLN1
1729_at823	L41690	0.001377	0.000812	0.000109	0.401776	TRADD
32173_at824	X95384	0.00482	0.000812	0.00053	0.327055	UK114
36000_at825	X98054	0.00482	0.001094	4.71E-05	-0.12615	CREBL1
271_s_at826	J05036	0.00482	0.001094	0.00171	0.064463	CTSE
40093_at827	AF001434	0.00482	0.001094	0.000161	-0.26223	EHD1
663_at828	L18960	0.00482	0.001094	3.26E-05	-0.38369	EIF1A
38340_at829	AB014555	0.00482	0.001094	0.001608	-0.18202	KIAA0655
36673_at830	X76057	0.00482	0.001094	0.000352	0.193745	MPI
1986_at831	X74594	0.00482	0.001094	0.000352	0.439326	RBL2
39857_at832	AF044309	0.00482	0.001094	0.000217	-0.2163	STX11
37911_at833	U07158	0.00482	0.001094	0.000122	-0.2301	STX4A
633_s_at834	L40386	0.00482	0.001094	7.97E-05	-0.19863	TFDP2
39513_at835	H97470	0.00482	0.001094	0.000624	-0.10587	
38213_at836	U78027	0.00482	0.001094	0.000804	0.340784	
1530_g_at837	U50534	0.001377	0.001345	0.00039	0.250627	13CDNA73
34181_at838	X55330	0.001377	0.001345	9.30E-05	0.493025	AGA
36637_at839	L19605	0.001377	0.001345	0.004442	0.183134	ANXA11
39082_at840	Y00097	0.001377	0.001345	4.42E-05	0.409932	ANXA6
2000_at841	U26455	0.00482	0.001345	0.000705	0.499049	ATM
34783_s_at842	AF047473	0.001377	0.001345	5.14E-05	0.226	BUB3
579_at843	M95724	0.00482	0.001345	0.002166	-0.46553	CENPC1
35852_at844	AB014558	0.001377	0.001345	0.004662	-0.44793	CRY2
41670_at845	R38263	0.001377	0.001345	0.00048	-0.12843	DJ347H13.4
36403_s_at846	AI434146	0.001377	0.001345	0.000397	0.187485	DKFZp570I0164
1306_at847	D12686	0.00482	0.001345	0.008744	-0.11456	EIF4G1
39542_at848	AF059611	0.00482	0.001345	0.000694	-0.27343	ENC1
40522_at849	X59834	0.001377	0.001345	0.004986	-0.34836	GLUL
319_s_at850	D64142	0.001377	0.001345	0.000169	0.293999	H1FX
36372_at851	U51333	0.001377	0.001345	0.000376	0.273402	HK3
235_at852	M59488	0.001377	0.001345	0.001357	-0.13313	HUMS100B3
41166_at853	X58529	0.001377	0.001345	0.000417	1.04789	IGHM
37695_at854	D79983	0.001377	0.001345	2.97E-05	0.387491	KIAA0161
40517_at855	AB002370	0.00482	0.001345	0.00052	0.425557	KIAA0372
33333_at856	AB007863	0.001377	0.001345	0.000128	0.29668	KIAA0403
39580_at857	AB014549	0.001377	0.001345	0.001505	0.42387	KIAA0649
37772_at858	AB020711	0.00482	0.001345	0.002079	0.222346	KIAA0904
34713_at859	AB002357	0.001377	0.001345	0.001045	0.317849	KIF3B
39232_at860	U09284	0.00482	0.001345	0.000792	-0.23635	LIMS1

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3542l_at~~861~~	D50810	0.001377	0.001345	5.17E-05	-0.1859	LNPEP
4151l_at~~862~~	U18259	0.001377	0.001345	0.000153	0.229322	MHC2TA
40877_s_at~~863~~	AF041080	0.00482	0.001345	0.001964	0.367098	MN7
4040b_at~~864~~	X70991	0.001377	0.001345	0.00203	-0.14032	NAB2
3383b_at~~865~~	AC002045	0.00482	0.001345	0.00028	0.326033	NPIP
3815b_at~~866~~	U92538	0.001377	0.001345	0.00149	0.2372	ORC5L
1560g_at~~867~~	U24153	0.001377	0.001345	0.00018	-0.36291	PAK2
3623p_at~~868~~	Z49194	0.001377	0.001345	0.000519	0.215733	POU2AF1
3835p_at~~869~~	AF016371	0.001377	0.001345	0.001059	0.240562	PPIH
3284s_at~~870~~	AF020736	0.001377	0.001345	6.26E-05	-0.32893	PSMC4
1760s_at~~871~~	D11327	0.001377	0.001345	0.00019	-0.74969	PTPN7
3525s_at~~872~~	AF098799	0.00482	0.001345	0.001893	-0.3646	RANBP7
1848s_at~~873~~	M22995	0.001377	0.001345	0.005586	0.270032	RAP1A
3154s_at~~874~~	L11566	0.001377	0.001345	0.000291	0.17032	RPL18
3443s_at~~875~~	U71364	0.001377	0.001345	0.000276	-0.24064	SERPINB9
3466s_at~~876~~	X07834	0.00482	0.001345	0.000362	-0.21917	SOD2
1634s_at~~877~~	X05839	0.001377	0.001345	0.000779	-0.20819	TGFB1
3523s_at~~878~~	AB000509	0.001377	0.001345	3.63E-05	0.460686	TRAF5
147_at~~879~~	U82130	0.001377	0.001345	4.69E-05	-0.36064	TSG101
283_at~~880~~	L16842	0.001377	0.001345	0.001533	0.189597	UQCRC1
4010s_at~~881~~	X51521	0.001377	0.001345	0.000379	-0.62845	VIL2
1235at~~882~~	M86400	0.001377	0.001345	0.000132	-0.30595	YWHAZ
3203t_at~~883~~	AF041259	0.001377	0.001345	0.001393	0.202001	ZNF217
3490s_g_at~~884~~	AA977136	0.001377	0.001345	0.001953	0.095364	
3623p_at~~885~~	AI624038	0.001377	0.001345	0.001833	-0.16137	
3564s_at~~886~~	AL050148	0.00482	0.001345	0.000905	0.266795	
1285at~~887~~	HG2709-HT2805	0.001377	0.001345	0.000134	-0.22645	
1162g_at~~888~~	HG3227-HT3404	0.001377	0.001345	4.02E-05	-0.23244	
3437s_at~~889~~	M28225	0.00482	0.001345	0.001444	-0.95152	
37277_at~~890~~	U80017	0.001377	0.001345	0.004917	0.171432	
36297_at~~891~~	X55544	0.001377	0.001467	0.001049	-0.12406	ATF1
3835t_at~~892~~	X52560	0.001377	0.001467	8.17E-05	-0.50375	CEBPB
4136p_at~~893~~	AA044787	0.001377	0.001467	0.001147	0.289086	CNOT8
4004l_at~~894~~	AF017790	0.001377	0.001467	6.88E-06	0.382661	HEC
771_s_at~~895~~	D00749	0.001377	0.001467	0.000131	-0.10539	HUMCD7G3
3193s_s_at~~896~~	AB007890	0.001377	0.001467	0.000838	0.200677	KIAA0430
3637l_at~~897~~	L35251	0.001377	0.001467	0.000873	0.12909	MFAP3
3274r_s_at~~898~~	AF098638	0.001377	0.001467	0.000684	-0.18761	RAB5EP
3532p_at~~899~~	AB004857	0.001377	0.001467	0.000471	0.23048	SLC11A2
4177s_at~~900~~	U53347	0.001377	0.001467	0.001367	-0.13658	SLC1A5
4041s_at~~901~~	U04847	0.001377	0.001467	0.000403	0.117176	SMARCB1
4044s_at~~902~~	M92843	0.001377	0.001467	3.30E-05	-1.37866	ZFP36
3400l_at~~903~~	AF033199	0.001377	0.001467	0.00019	0.237743	ZNF204
37504_at~~904~~	AC004893	0.001377	0.001467	0.000617	-0.25759	
3850s_at~~905~~	AL050151	0.001377	0.001467	8.03E-06	-0.80887	

31771_at906	U80770	0.001377	0.001467	0.006738	-0.12644	
31665_s_at907	W27675	0.00482	0.001614	0.005157	0.468709	CDA02
35233_r_at908	AI056696	0.00482	0.001614	0.000665	0.215941	CETN3
39723_at909	AF062536	0.00482	0.001614	0.005001	0.197482	CUL1
38791_at910	D29643	0.00482	0.001614	0.0005	0.157183	DDOST
35972_at911	AA181196	0.00482	0.001614	0.000166	0.119162	FLJ11712
35261_at912	W07033	0.001377	0.001614	0.000136	0.347648	GMFG
34571_at913	Z18859	0.00482	0.001614	0.000684	0.181514	GNAT2
1931_at914	U83660	0.00482	0.001614	0.00114	0.136411	HSU83660
38823_s_at915	AA628946	0.00482	0.001614	0.002684	0.337197	KHSRP
33462_at916	D13626	0.00482	0.001614	0.005837	0.254138	KIAA0001
32660_at917	AB002340	0.00482	0.001614	0.002977	0.168464	KIAA0342
32203_at918	AB002353	0.001377	0.001614	0.000119	0.305921	KIAA0355
36472_at919	U32849	0.00482	0.001614	0.000272	0.345048	NMI
1348_s_at920	S79219	0.00482	0.001614	0.000119	0.167463	PCCA
1486_at921	L37127	0.00482	0.001614	0.010173	0.103446	POLR2J
32776_at922	M35416	0.00482	0.001614	0.001433	0.33505	RALB
32597_at923	X76061	0.00482	0.001614	0.000273	0.378113	RBL2
40782_at924	AF061741	0.00482	0.001614	0.004586	0.221278	SDR1
34189_at925	D31891	0.001377	0.001614	0.000819	0.161458	SETDB1
32161_at926	W26406	0.00482	0.001614	0.000479	0.300512	SIAH1
802_at927	X84002	0.00482	0.001614	0.000699	0.143479	TAF2J
34307_at928	U81006	0.00482	0.001614	0.003151	0.255479	TM9SF2
1328_at929	U69108	0.00482	0.001614	0.000657	0.208286	TRAF5
31613_at930	S66666	0.00482	0.001614	0.002417	0.119478	
1211_s_at931	U84388	0.00482	0.001719	0.000197	-0.18606	CRADD
39113_at932	L08069	0.00482	0.001719	0.001985	-0.31866	DNAJA1
38041_at933	U41514	0.00482	0.001719	9.38E-05	-0.44803	GALNT1
40562_at934	M69013	0.001377	0.001719	6.26E-05	-0.1948	GNA11
38320_s_at935	L11706	0.00482	0.001719	0.001422	-0.16675	LIPE
36130_f_at936	R92331	0.00482	0.001719	0.000198	-0.24196	MT1E
37544_at937	X64318	0.00482	0.001719	0.006253	-0.37391	NFIL3
40360_at938	X12458	0.00482	0.001719	0.001489	-0.33668	P3
1265_g_at939	M25393	0.00482	0.001719	0.000958	-0.23304	PTPN2
595_at940	M59465	0.00482	0.001719	0.0002	-0.96074	TNFAIP3
34323_at941	AF084260	0.00482	0.001719	0.001063	-0.39491	TRIP15
733_at942	HG2149-HT2219	0.00482	0.001719	0.001437	-0.14432	
39153_at943	AB021663	0.00482	0.001963	0.00027	-0.13923	ATF5
39692_at944	AL080209	0.00482	0.001963	0.000337	0.437957	DKFZP586F2423
2056_at945	M34641	0.00482	0.001963	0.002352	-0.14552	FGFR1
38710_at946	AL096714	0.001377	0.001963	0.000469	0.224782	FLJ20113
38243_at947	AB011124	0.001377	0.001963	0.000101	-0.17709	KIAA0552
40492_at948	AB020633	0.001377	0.001963	0.00082	0.308616	KIAA0826
33210_at949	AB029020	0.001377	0.001963	0.00061	0.3824	KIAA1097
38051_at950	X76220	0.001377	0.001963	7.21E-05	0.444366	MAL

34482_at951	AF040964	0.00482	0.001963	0.001161	-0.54746	MGC4701
41475_at952	U91512	0.001377	0.001963	0.00035	-0.55826	NINJ1
1014_at953	U60325	0.00482	0.001963	0.000288	-0.14386	POLG
362_at954	Z15108	0.001377	0.001963	0.000107	0.176424	PRKCZ
36998_s_at955	Y08262	0.001377	0.001963	0.000183	0.377974	SCA2
37428_at956	U30246	0.001377	0.001963	0.000209	-0.25952	SLC12A2
35298_at957	J04137	0.001377	0.001963	0.000641	-0.22175	SSA2
1830_s_at958	M38449	0.001377	0.001963	0.0004	-0.29059	TGFB1
36531_r_at959	AC005757	0.00482	0.001963	0.000169	0.387439	
919_at960	HG825-HT825	0.001377	0.001963	0.000553	-0.19964	
39590_at961	AF047348	0.001377	0.002207	0.000292	0.202669	APBA2
31877_at962	AF053977	0.001377	0.002207	0.003143	0.134266	CDC23
38345_at963	AF083322	0.001377	0.002207	0.000344	0.272282	CEP1
40905_s_at964	AL050369	0.001377	0.002207	0.001224	0.241992	DKFZP566J153
36188_at965	D32257	0.001377	0.002207	0.000238	0.300058	GTF3A
32087_at966	M65217	0.001377	0.002207	0.000232	0.249614	HSF2
31826_at967	AB014574	0.001377	0.002207	0.000606	0.130056	KIAA0674
41179_at968	AB029023	0.001377	0.002207	0.000219	0.219428	KIAA1100
38390_at969	Z34975	0.001377	0.002207	8.88E-05	0.41432	LDLC
40715_at970	D83597	0.001377	0.002207	0.000136	0.249838	LY64
38431_at971	U09759	0.001377	0.002207	0.000842	0.330751	MAPK9
484_at972	U59302	0.001377	0.002207	0.000241	0.309348	NCOA1
36008_at973	AJ005698	0.001377	0.002207	0.004173	0.139618	PARN
37362_at974	X54871	0.001377	0.002207	0.010035	0.119258	RAB5B
35722_at975	AL080198	0.001377	0.002207	0.002866	0.251598	RENT2
39988_at976	M74447	0.001377	0.002207	0.000444	0.093537	TAP2
40854_at977	J04973	0.001377	0.002207	0.011696	0.141705	UQCRC2
38370_at978	U90902	0.001377	0.002207	0.001336	0.246217	
35036_at979	U94333	0.001377	0.002323	0.004818	-0.13898	C1QR
40218_at980	U60808	0.001377	0.002323	0.000374	-0.12217	CDS1
276_at981	L08069	0.001377	0.002323	0.002161	-0.29982	DNAJA1
38706_at982	AA552140	0.001377	0.002323	0.003368	-0.22604	E2F4
587_at983	M31210	0.001377	0.002323	0.000124	-0.33555	EDG1
37018_at984	AI189287	0.001377	0.002323	0.002445	-0.24115	H1F2
33368_at985	W25934	0.001377	0.002323	0.003385	-0.32382	JTV1
34860_g_at986	Z98046	0.001377	0.002323	0.000122	-0.33551	MAGED2
37505_at987	L76571	0.001377	0.002323	0.009985	-0.12617	NR0B2
39859_r_at988	AF071504	0.001377	0.002323	0.000191	-0.14267	STX11
38795_s_at989	X56687	0.001377	0.002323	0.00011	-0.29728	UBTF
38245_i_at990	AI097085	0.001377	0.002323	0.000941	-0.16209	
36638_at991	AA114830	0.001377	0.002503	0.000293	0.272601	AKAP10
39094_at992	AI991631	0.001377	0.002503	0.000132	-0.11786	BRD4
36270_at993	U04343	0.001377	0.002503	4.45E-05	-0.25478	CD86
40699_at994	M12824	0.001377	0.002503	0.008271	-0.34597	CD8A
446_at995	U89896	0.001377	0.002503	0.006997	-0.2182	CSNK1G2

39593_at996	AI432401	0.001377	0.002503	0.006072	0.32631	FGL2
40486_g_at997	AA176780	0.001377	0.002503	0.001296	0.14235	HSA249128
31840_at998	M21188	0.001377	0.002503	0.000165	0.251899	IDE
41596_s_at999	U43572	0.001377	0.002503	0.000128	0.318327	NAGLU
1539_at1000	X02751	0.001377	0.002503	0.000359	-0.2229	NRAS
34397_at1001	AF069250	0.001377	0.002503	0.00135	0.476217	OA48-18
39176_at1002	D25328	0.001377	0.002503	0.000171	0.125335	PFKP
37024_at1003	AF010312	0.001377	0.002503	0.001216	-0.47628	PIG7
1496_at1004	M34668	0.001377	0.002503	0.000421	0.181315	PTPRA
39601_at1005	AF061836	0.001377	0.002503	0.001026	0.21847	RASSF1
33369_at1006	AI535653	0.001377	0.002503	0.001712	0.34571	SC4MOL
36112_r_at1007	X75755	0.001377	0.002503	0.003813	-0.2236	SFRS2
35270_at1008	W16505	0.001377	0.002503	0.001699	0.101763	SNRPD2
37074_at1009	L31529	0.001377	0.002503	0.000325	0.144265	SNTB1
36940_at1010	D86970	0.001377	0.002503	0.000219	0.218777	TIAF1
32254_at1011	AL050223	0.001377	0.002503	0.002632	0.2458	VAMP2
35916_s_at1012	AA877215	0.001377	0.002503	0.008439	-0.17878	
38510_at1013	AL049435	0.001377	0.002503	0.000111	0.194323	
40201_at1014	M76180	0.001377	0.002575	0.000698	0.162775	DDC
33195_at1015	M94065	0.001377	0.002575	0.000426	0.156894	DHODH
1161_at1016	J04988	0.001377	0.002575	6.17E-05	-0.22304	HSPCB
36574_at1017	Z68907	0.001377	0.002575	0.000305	0.391111	IDH3G
39728_at1018	J03909	0.001377	0.002575	0.000837	-0.35709	IFI30
34192_at1019	AB011104	0.001377	0.002575	0.000729	0.227798	KIAA0532
41122_at1020	AB011173	0.001377	0.002575	0.000585	0.283714	KIAA0601
40463_at1021	U70322	0.001377	0.002575	0.000177	-0.41259	KPNB2
37542_at1022	D86961	0.001377	0.002575	0.001925	-0.19403	LHFPL2
38956_at1023	AF052111	0.001377	0.002575	0.000738	0.249468	LOC51172
32051_at1024	AJ224875	0.001377	0.002575	0.005091	0.139606	MGC2840
1406_at1025	M21985	0.001377	0.002575	0.001409	-0.102	NR2C1
1594_at1026	J05448	0.001377	0.002575	0.004982	-0.15329	POLR2C
38011_at1027	AB006572	0.001377	0.002575	0.000169	0.213636	RMP
36113_s_at1028	AJ011712	0.001377	0.002575	0.011372	0.066711	TNNT1
39134_at1029	AJ006973	0.001377	0.002575	0.000101	-0.31773	TOM1
457_s_at1030	U67122	0.001377	0.002575	0.000364	-0.14274	UBL1
40691_at1031	U71598	0.001377	0.002575	0.003508	0.128607	ZNF274
37707_i_at1032	M81118	0.001377	0.002575	0.00023	0.333526	
488_at1033	U61166	0.001377	0.002575	0.003055	-0.14488	
31616_r_at1034	U94902	0.001377	0.002575	0.000137	-0.23298	
33802_at1035	Z82244	0.001377	0.002575	0.000258	-0.53938	
36586_at1036	M36341	0.001377	0.002788	0.00056	-0.38498	ARF4
37309_at1037	L09159	0.001377	0.002788	0.00112	0.474985	ARHA
459_s_at1038	U68485	0.00482	0.002788	0.006797	0.224774	BIN1
41200_at1039	Z22555	0.001377	0.002788	0.005455	-0.16351	CD36L1
38976_at1040	D44497	0.00482	0.002788	0.004453	0.131654	CORO1A
40184_at1041	L37042	0.00482	0.002788	0.000582	-0.33273	CSNK1A1

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31823_at1042	M74099	0.001377	0.002788	0.00014	0.389638	CUTL1
35377_at1043	AL080159	0.001377	0.002788	0.002335	-0.11101	DKFZP434M154
32807_at1044	AF004292	0.001377	0.002788	0.001306	-0.2375	DKFZP566C134
38632_at1045	AF088982	0.001377	0.002788	0.001264	-0.22098	DNAJB5
39983_at1046	U73704	0.001377	0.002788	0.001412	-0.17508	FAP48
1071_at1047	M77810	0.00482	0.002788	0.000209	-0.15854	GATA2
33977_at1048	U67369	0.00482	0.002788	0.00347	0.137095	GFI1
770_at1049	D00632	0.001377	0.002788	0.001138	-0.15517	GPX3
41833_at1050	X99270	0.001377	0.002788	0.00065	0.191612	HSXQ28ORF
37040_at1051	D42041	0.00482	0.002788	0.003705	0.195279	KIAA0088
34359_at1052	AA524058	0.001377	0.002788	0.000288	0.360599	LOC51020
820_at1053	U77604	0.001377	0.002788	0.00233	0.296247	MGST2
674_s_at1054	J04031	0.00482	0.002788	0.000148	0.290038	MTHFD1
31883_at1055	AF025794	0.001377	0.002788	0.006763	0.107466	MTRR
37356_r_at1056	D86326	0.001377	0.002788	0.008217	0.124987	P115
34254_at1057	U14417	0.001377	0.002788	0.000521	-0.13999	RALGDS
1020_s_at1058	U85611	0.001377	0.002788	0.000126	-0.3879	SIP2-28
454_at1059	U66617	0.001377	0.002788	0.001462	-0.14653	SMARCD1
32574_at1060	X59960	0.001377	0.002788	0.005127	-0.11069	SMPD1
40262_at1061	AF031166	0.001377	0.002788	0.001219	0.110457	SRP46
1701_at1062	U86136	0.001377	0.002788	0.000542	0.149235	TEP1
37460_at1063	U16296	0.001377	0.002788	0.00138	0.136848	TIAM1
37312_at1064	D50917	0.001377	0.002788	0.000467	0.402091	TRIP-Br2
34224_at1065	AC004770	0.001377	0.002788	0.001042	-0.10615	
31493_s_at1066	J03071	0.001377	0.002788	0.0116	0.17732	
33102_at1067	D67031	0.00482	0.004163	0.000204	0.543743	ADD3
458_at1068	U68030	0.00482	0.004163	0.000279	-0.16075	CCR6
40490_at1069	U41387	0.00482	0.004163	8.67E-05	-0.29576	DDX21
34240_at1070	AF084535	0.00482	0.004163	0.002306	0.159095	EPM2A
35983_i_at1071	AI417075	0.00482	0.004163	0.000538	0.330385	FLJ14040
38811_at1072	D82348	0.00482	0.004349	0.006063	0.245422	ATIC
38084_at1073	AA648295	0.00482	0.004349	0.002422	0.337484	CBX3
34723_at1074	U79270	0.00482	0.004349	0.001345	0.460807	COX11
39846_at1075	AF071748	0.00482	0.004349	0.002471	0.170315	CTSF
40341_at1076	AL080088	0.00482	0.004349	0.000207	0.165357	DKFZP564K2062
41234_at1077	AI540318	0.00482	0.004349	0.00055	-0.13789	DNAJB6
38012_at1078	U03272	0.00482	0.004349	0.003893	0.101031	FBN2
40479_at1079	Z97989	0.00482	0.004349	0.001126	-0.41969	FYN
39913_at1080	AF042379	0.00482	0.004349	0.008308	0.176604	GCP2
1017_at1081	U73737	0.00482	0.004349	0.00262	-0.14396	HUMMSH06
38483_s_at1082	AF031167	0.00482	0.004349	0.000117	0.201914	IL15
34221_at1083	D83778	0.00482	0.004349	0.000504	-0.2149	KIAA0194
35789_at1084	AB028965	0.00482	0.004349	0.007277	0.125446	KIAA1042
2024_s_at1085	M79321	0.00482	0.004349	0.003247	-0.21992	LYN
1130_at1086	L11284	0.00482	0.004349	0.003994	-0.09508	MAP2K1

36118_at1087	AJ000882	0.00482	0.004349	0.00042	0.180413	NCOA1
40822_at1088	L41067	0.00482	0.004349	0.000388	0.370635	NFATC3
36146_at1089	AF057297	0.00482	0.004349	0.001191	0.521103	OAZ2
39873_at1090	X66360	0.00482	0.004349	0.001123	-0.17473	PCTK2
36196_at1091	U24183	0.00482	0.004349	0.001156	0.141168	PFKM
903_at1092	L42373	0.00482	0.004349	0.006706	0.165885	PPP2R5A
40824_at1093	AB018288	0.00482	0.004349	0.003777	0.184227	RANBP16
41214_at1094	M58459	0.00482	0.004349	0.008923	-1.04752	RPS4Y
2037_s_at1095	M60725	0.00482	0.004349	0.001349	-0.10092	RPS6KB1
32402_s_at1096	Y10931	0.00482	0.004349	0.001246	0.194156	SPK
40963_at1097	AB004904	0.00482	0.004349	0.000233	-0.31373	SSI-3
31863_at1098	AF060798	0.00482	0.004349	0.000809	0.142845	STK16
38480_s_at1099	U66867	0.00482	0.004349	0.011318	0.150812	UBE2I
35847_at1100	AB028980	0.00482	0.004349	0.001471	0.265042	USP24
38262_at1101	AF052107	0.00482	0.004349	0.002884	0.197902	
35557_at1102	AL031985	0.00482	0.004349	0.000181	-0.24089	
35440_g_at1103	D26121	0.00482	0.004349	0.00387	-0.16268	
34036_at1104	W28667	0.00482	0.004349	0.004391	0.476395	
34833_at1105	AL050157	0.00482	0.004467	0.000289	0.269949	DKFZP586O0120
38363_at1106	U31930	0.00482	0.004467	0.000244	0.349997	DUT
41333_at1107	AI951946	0.00482	0.004467	8.71E-05	0.401112	HBOA
35650_at1108	AB002354	0.00482	0.004467	0.001517	-0.13368	KIAA0356
1376_at1109	M36067	0.00482	0.004467	8.15E-05	0.277858	LIG1
691_g_at1110	J02783	0.00482	0.004467	0.002151	-0.21979	P4HB
1085_s_at1111	M37238	0.00482	0.004467	0.005333	-0.15474	PLCG2
38234_at1112	M99438	0.00482	0.004467	6.20E-05	-0.36844	TLE3
33386_at1113	Z97630	0.00482	0.004467	0.002794	0.217849	
34777_at1114	D14874	0.00482	0.005608	0.000611	-0.55358	ADM
931_at1115	L08177	0.00482	0.005608	0.000434	-0.49252	EBI2
36581_at1116	U09510	0.00482	0.005608	5.27E-05	-0.57567	GARS
1126_s_at1117	L05424	0.00482	0.005608	0.000114	-0.39048	HUMSCG19
35135_at1118	X13956	0.00482	0.005608	0.004098	0.187622	MGC10471
38335_at1119	U88620	0.00482	0.005608	0.00074	0.345628	OGG1
39780_at1120	M29551	0.00482	0.005608	0.000471	0.319301	PPP3CB
39604_at1121	AF068836	0.00482	0.005608	0.000323	-0.23628	PSCDBP
33229_at1122	U08316	0.00482	0.005608	0.0006	0.205899	RPS6KA3
32822_at1123	J02966	0.00482	0.005608	0.000498	-0.11291	SLC25A4
38040_at1124	AF107463	0.00482	0.005608	0.002824	-0.36924	SPF30
33124_at1125	AB000450	0.00482	0.005608	0.000256	-0.24717	VRK2
40760_at1126	AF070590	0.00482	0.005608	0.000834	0.127523	
32233_at1127	AF001383	0.00482	0.006065	0.002075	0.16512	BIN1
32594_at1128	AF026291	0.00482	0.006065	0.000385	-0.16859	CCT4
37642_at1129	D63877	0.00482	0.006065	0.005226	-0.13956	KIAA0157
191_at1130	U14383	0.00482	0.006065	0.002623	-0.18669	MUC8
40285_at1131	U68140	0.00482	0.006065	0.000677	0.172443	NVL

ANNOTATED MARKED-UP SPECIFICATION

1275_at~~1132~~	L25441	0.00482	0.006065	0.000613	-0.17207	PGGT1B
40898_at~~1133~~	U46751	0.00482	0.006065	0.000578	-0.38675	SQSTM1
1149_at~~1134~~	HG4740-HT5187	0.00482	0.006065	0.00867	0.146562	
38864_at~~1135~~	W26851	0.00482	0.006065	0.002052	0.312992	
35183_at~~1136~~	U78735	0.00482	0.006347	0.000529	-0.09197	ABCA3
35274_at~~1137~~	Y12226	0.00482	0.006347	0.000397	-0.21303	AP1G1
37237_at~~1138~~	D38293	0.00482	0.006347	0.002894	-0.24373	AP3M2
31870_at~~1139~~	X14046	0.00482	0.006347	0.001084	0.134786	CD37
40174_at~~1140~~	AF026004	0.00482	0.006347	0.008622	-0.07494	CLCN2
38916_at~~1141~~	U46023	0.00482	0.006347	0.000273	-0.17969	CXorf6
39607_at~~1142~~	AL080178	0.00482	0.006347	0.000683	0.260343	DKFZP434K171
41437_at~~1143~~	AL080118	0.00482	0.006347	0.001904	-0.28696	DKFZP564F1123
34821_at~~1144~~	AL050197	0.00482	0.006347	0.004294	0.233045	DKFZP586D0623
1005_at~~1145~~	X68277	0.00482	0.006347	0.011411	-0.42385	DUSP1
38042_at~~1146~~	X03674	0.00482	0.006347	0.008478	0.174463	G6PD
35307_at~~1147~~	Y13286	0.00482	0.006347	0.004068	0.134985	GDI2
1038_s_at~~1148~~	U19247	0.00482	0.006347	0.000589	-0.29688	HSINFGRA7
35973_at~~1149~~	AB023163	0.00482	0.006347	0.002537	0.194491	HYPH
36598_s_at~~1150~~	L36818	0.00482	0.006347	0.007182	0.204818	INPPL1
36465_at~~1151~~	U51127	0.00482	0.006347	0.003952	0.108702	IRF5
37913_at~~1152~~	M15395	0.00482	0.006347	0.001863	0.402323	ITGB2
35755_at~~1153~~	U51336	0.00482	0.006347	0.008615	0.336527	ITPK1
39222_at~~1154~~	AJ000008	0.00482	0.006347	0.000256	-0.14181	PIK3C2G
33150_at~~1155~~	AI126004	0.00482	0.006347	0.000954	0.262925	SAS10
34432_at~~1156~~	AF051325	0.00482	0.006347	0.000144	-0.43952	SH2D2A
33879_at~~1157~~	U79528	0.00482	0.006347	0.002518	0.158101	SR-BP1
36900_at~~1158~~	U52426	0.00482	0.006347	9.31E-05	0.411984	STIM1
38113_at~~1159~~	AB018339	0.00482	0.006347	0.000751	0.199758	SYNE-1B
33873_at~~1160~~	D43642	0.00482	0.006347	0.0005	0.305805	TCFL1
37056_at~~1161~~	D29767	0.00482	0.006347	0.003934	-0.09702	TEC
31481_s_at~~1162~~	M92383	0.00482	0.006347	0.001466	0.219769	TMSB10
35813_at~~1163~~	AA192359	0.00482	0.006347	0.00028	0.17619	TRN-SR
33842_at~~1164~~	AC004472	0.00482	0.006347	0.002169	-0.15115	
41841_at~~1165~~	AF052138	0.00482	0.006347	0.000189	0.441167	
31997_at~~1166~~	X15674	0.00482	0.006347	0.007899	-0.10738	
39733_at~~1167~~	Z82215	0.00482	0.006347	0.002527	0.153792	
39091_at~~1168~~	AF070523	0.00482	0.006634	0.00037	0.437983	JWA
36193_at~~1169~~	D13641	0.00482	0.006634	0.000776	0.275308	KIAA0016
36142_at~~1170~~	X79204	0.00482	0.006634	0.000182	0.256049	SCA1
40420_at~~1171~~	AB015718	0.00482	0.006634	0.001172	0.202412	STK10
33020_at~~1172~~	AF059575	0.00482	0.006634	0.000563	-0.18074	
37178_at~~1173~~	M74089	0.00482	0.006634	0.00076	0.187888	
37604_at~~1174~~	U44111	0.00482	0.006634	0.003845	0.105361	
40979_at~~1175~~	AJ243310	0.00482	0.006921	0.000945	-0.97643	C14orf3
35806_at~~1176~~	W26854	0.00482	0.006921	0.011098	-0.13774	DKFZP434D156

148_at~~1177~~	U88629	0.00482	0.006921	0.001778	-0.16763	ELL2
3169_at~~1178~~	M59830	0.00482	0.006921	0.000221	-1.12882	HSPA1B
4012_at~~1179~~	M95929	0.00482	0.006921	0.004606	-0.34536	PMX1
234_s_at~~1180~~	M57399	0.00482	0.006921	0.010231	-0.14331	PTN
3738_at~~1181~~	N25117	0.00482	0.006921	0.002068	-0.16335	RPS26
3773_at~~1182~~	AL049940	0.00482	0.006921	0.001149	-0.42489	RYBP
3908_at~~1183~~	U39318	0.00482	0.006921	0.001097	-0.24533	UBE2D3
369_s_at~~1184~~	Z29331	0.00482	0.006921	0.000193	-0.15851	UBE2H
233_s_at~~1185~~	M55682	0.00482	0.006921	0.010264	-0.10921	
3674_at~~1186~~	S58544	0.00482	0.006921	0.005501	-0.11193	
3189_at~~1187~~	L13687	0.00482	0.007311	0.002185	0.114008	ARL2
3930_at~~1188~~	M88714	0.00482	0.007311	0.002075	0.114833	BDKRB2
3210_at~~1189~~	AL050173	0.00482	0.007311	0.001866	0.128954	C21orf25
3528_r_at~~1190~~	M33680	0.00482	0.007311	0.002612	0.134487	CD81
3793_at~~1191~~	X05299	0.00482	0.007311	0.003837	0.171613	CENPB
3702_at~~1192~~	X16832	0.00482	0.007311	0.000578	0.177395	CTSH
3789_at~~1193~~	U83410	0.00482	0.007311	0.005207	0.219569	CUL2
3687_at~~1194~~	AL050018	0.00482	0.007311	0.003938	0.220539	DKFZP564B116
3645_at~~1195~~	AL080063	0.00482	0.007311	0.006562	0.186332	DKFZP564I052
3696_at~~1196~~	AL050286	0.00482	0.007311	0.000767	0.221397	DKFZP586A011
3733_at~~1197~~	X63692	0.00482	0.007311	0.003174	0.172997	DNMT1
3936_at~~1198~~	AA522537	0.00482	0.007311	0.002762	0.113812	ELAC2
3594_at~~1199~~	AI183417	0.00482	0.007311	0.006167	0.101739	GABPB1
3806_at~~1200~~	X62534	0.00482	0.007311	0.000973	0.195089	HMG2
3356_at~~1201~~	D50532	0.00482	0.007311	0.001268	0.159735	HML2
3752_at~~1202~~	AJ006591	0.00482	0.007311	0.001379	0.1682	HSA6591
3854_at~~1203~~	Y00796	0.00482	0.007311	0.000438	0.386166	ITGAL
3423_at~~1204~~	AB018301	0.00482	0.007311	0.008701	0.138344	KIAA0758
3703_at~~1205~~	AB020694	0.00482	0.007311	0.002526	0.205561	KIAA0887
3208_at~~1206~~	AB023198	0.00482	0.007311	0.000409	0.275051	KIAA0981
3421_at~~1207~~	AB028958	0.00482	0.007311	0.001533	0.117614	KIAA1035
3736_at~~1208~~	U66711	0.00482	0.007311	0.006567	0.260368	LY6E
3597_at~~1209~~	L13744	0.00482	0.007311	0.007658	0.19599	MLLT3
3601_at~~1210~~	Y09631	0.00482	0.007311	0.000769	0.309898	PIBF1
3562_at~~1211~~	L77213	0.00482	0.007311	0.001122	0.247214	PMVK
3912_f_at~~1212~~	X73478	0.00482	0.007311	0.000681	0.242238	PPP2R4
3924_s_at~~1213~~	U94319	0.00482	0.007311	0.000688	0.337656	PSIP2
1043_s_at~~1214~~	U27516	0.00482	0.007311	0.000222	0.194938	RAD52
3796_at~~1215~~	W25793	0.00482	0.007311	0.000438	0.258505	RNF3
3233_at~~1216~~	X06617	0.00482	0.007311	0.002581	0.116631	RPS11
3464_at~~1217~~	Z25749	0.00482	0.007311	0.001419	0.123333	RPS7
3864_at~~1218~~	U80760	0.00482	0.007311	0.007371	0.161214	TNRC1
3349_at~~1219~~	L27071	0.00482	0.007311	0.000638	0.372837	TXK
3603_at~~1220~~	AL031427	0.00482	0.007311	0.000541	0.367004	
3851_at~~1221~~	AL109722	0.00482	0.007311	0.00187	0.134304	
3558_at~~1222~~	X15675	0.00482	0.007311	0.011165	0.131908	

37971_at1223	AL050089	0.00482	0.007852	0.001906	-0.23061	BAZ1A
1274_s_at1224	L22005	0.00482	0.007852	0.002439	-0.22532	CDC34
37960_at1225	AB014679	0.00482	0.007852	0.003059	-0.13664	CHST2
366183_g_at1226	X77956	0.00482	0.007852	0.000689	-0.22743	ID1
32534_f_at1227	AI814466	0.00482	0.007852	0.001127	-0.1955	VAMP5
1516_g_at1228	HG4074-HT4344	0.00482	0.007852	0.000964	-0.17461	
38703_at1229	AF005050	0.00482	0.008059	0.001761	0.230395	DNPEP
925_at1230	J03909	0.00482	0.008059	0.000125	-0.18353	IFI30
32696_at1231	X59841	0.00482	0.008059	0.000226	0.265756	PBX3
37774_at1232	AI819942	0.00482	0.009314	0.002286	0.326115	02-Sep
38470_i_at1233	D86981	0.00482	0.009314	0.003441	0.319525	APPBP2
32825_at1234	Y10805	0.00482	0.009314	0.002583	0.183496	HRMT1L2
478_g_at1235	U51127	0.00482	0.009314	0.00212	0.282678	IRF5
32437_at1236	U14970	0.00482	0.009314	0.000561	0.144991	RPS5
33813_at1237	AI813532	0.00482	0.009314	0.00037	-0.41933	TNFRSF1B
39955_at1238	Y15228	0.00482	0.010363	0.002026	-0.17032	DLEU2
40982_at1239	AA926957	0.00482	0.010363	0.000909	-0.22483	FLJ10534
40925_at1240	AA554945	0.00482	0.010363	0.001827	-0.14301	FLJ10803
34039_at1241	AJ001383	0.00482	0.010363	0.001968	-0.3226	LY94
40199_at1242	M97676	0.00482	0.010363	0.010011	-0.16313	MSX1
980_at1243	AF002020	0.00482	0.010363	0.001278	-0.1736	NPC1
1245_i_at1244	U25975	0.00482	0.010363	0.000764	-0.24651	PAK2
1225_g_at1245	X66363	0.00482	0.010363	0.000837	-0.4179	PCTK1
722_at1246	D87957	0.00482	0.010363	0.004418	-0.14751	RQCD1
32633_s_at1247	AI610467	0.00482	0.010363	0.000699	-0.17683	SMG1
38621_at1248	AJ012008	0.00482	0.010363	0.002571	-0.32997	
36131_at1249	AJ012008	0.00482	0.010363	0.001638	-0.16204	

Table II: Gene Expression Profile from PBMCs of MS vs. Healthy- Highest Scoring Genes (Bonfferoni analysis)

SEQ ID NO:	*Affymetrix ID no:*	Identifier	TNOM PValue	Info PValue	t-Test PValue	Log FoldChange	Symbol
271	32213_at1250	AA203527	1.37E-05	1.61E-06	1.18E-07	0.281992	RPP20
272	40615_at1251	AA780049	7.44E-05	2.35E-05	7.39E-07	0.54912	FLJ21439
273	37348_s_at1252	AA845349	7.44E-05	0.0001187	7.78E-07	0.457176	TRIP7
274	39388_at1253	AA902713	2.11E-06	1.99E-06	1.44E-06	0.474378	
243	4138	AB002344	7.44E-05	5.92E-05	8.48E-07	-1.00068	KIAA0

	6_i_at1254						346
154	39797_at1255	AB002347	2.11E-06	1.33E-07	7.19E-10	0.371731	KIAA0349
244	34661_at1256	AB002348	1.37E-05	3.86E-06	2.49E-07	0.576346	KIAA0350
155	32259_at1257	AB002386	2.11E-06	7.73E-07	5.34E-09	0.586117	EZH1
184	36260_at1258	AB002448	1.37E-05	5.01E-06	2.45E-07	0.468926	
183	40431_at1259	AB007891	1.37E-05	3.86E-06	3.99E-05	0.196376	KIAA0431
173	39650_s_at1260	AB007895	1.37E-05	5.01E-06	9.61E-07	0.186643	KIAA0435
257	32253_at1261	AB007927	2.11E-06	1.99E-06	2.12E-07	0.323787	RERE
254	39691_at1262	AB007960	2.11E-06	9.54E-07	7.96E-06	0.447772	SH3GLB1
182	34435_at1263	AB008775	0.0003443	0.0003041	1.88E-06	-0.80745	AQP9
194	41242_at1264	AB011004	0.0003443	7.05E-06	1.41E-06	-1.34073	UAP1
186	32784_at1265	AB011108	1.37E-05	5.05E-07	4.39E-07	0.453498	PRP4
258	41430_at1266	AB011113	1.37E-05	7.05E-06	3.74E-07	0.444795	WDR7
187	41077_at1267	AB011115	1.37E-05	5.05E-07	3.39E-07	0.382809	KIAA0543
188	32133_at1268	AB011161	2.57E-08	4.01E-09	9.64E-11	0.63432	PIP5K1C
197	38854_at1269	AB014535	1.37E-05	5.05E-07	1.04E-06	0.285282	KIAA0635
245	37375_at1270	AB014538	0.0003443	4.67E-05	1.98E-06	-0.63923	KIAA0638
246	35317_at1271	AB014579	1.37E-05	5.01E-06	6.08E-08	0.367966	MGEA5
251	4161	AB014608	7.44E-05	9.64E-05	4.59E-06	0.41494	KIAA0

	4_at~~1~~ ~~272~~						708
214	37760_at~~1~~ ~~273~~	AB015019	7.44E-05	7.05E-06	2.75E-07	-0.24515	BAIAP2
210	38873_at~~1~~ ~~274~~	AB018343	1.84E-09	4.16E-10	9.05E-12	0.383078	KIAA0800
223	41431_at~~1~~ ~~275~~	AB023153	2.11E-06	1.33E-07	1.82E-08	0.895842	KIAA0936
255	36458_at~~1~~ ~~276~~	AB023235	7.44E-05	1.61E-06	1.43E-05	0.311216	KIAA1018
240	32350_at~~1~~ ~~277~~	AB026118	0.0013772	0.0001897	4.47E-06	-0.24886	MALT1
235	38555_at~~1~~ ~~278~~	AB026436	7.44E-05	1.61E-06	0.000219	-0.7589	DUSP10
247	39417_at~~1~~ ~~279~~	AB028951	2.64E-07	1.72E-07	8.78E-09	0.543028	KIAA1028
248	37571_at~~1~~ ~~280~~	AB028981	2.11E-06	7.73E-07	5.34E-07	0.282288	KIAA1058
239	41796_at~~1~~ ~~281~~	AB029015	2.64E-07	2.49E-07	5.37E-09	0.695063	PLCE2
256	36862_at~~1~~ ~~282~~	AB029038	7.44E-05	1.61E-06	7.62E-05	0.364386	KIAA1115
167	39975_at~~1~~ ~~283~~	AC002400	1.37E-05	3.06E-05	2.28E-06	-0.25834	UBPH
151	358_at~~128~~ 4	AF000545	7.44E-05	5.23E-05	3.48E-06	-0.85393	P2Y10
152	31888_s_at~~128~~ ~~5~~	AF001294	1.37E-05	7.05E-06	1.23E-06	-0.76359	TSSC3
159	35926_s_at~~128~~ ~~6~~	AF004230	2.64E-07	1.72E-07	3.06E-07	0.349166	LILRB1
153	38270_at~~1~~ ~~287~~	AF005043	7.44E-05	5.23E-05	2.70E-06	0.408592	PARG
178	37819_at~~1~~ ~~288~~	AF007130	2.11E-06	5.05E-07	2.51E-06	0.391811	LOC54104
179	38764_at~~1~~ ~~289~~	AF007142	0.0003443	0.0004443	3.15E-06	0.678734	

180	35273_at1290	AF007151	1.37E-05	5.05E-07	3.25E-06	0.468343	MMS19L
156	1857_at1291	AF010193	7.44E-05	2.35E-05	1.26E-07	-1.4705	MADH7
176	36079_at1292	AF010309	1.37E-05	5.01E-06	7.36E-07	-0.28533	PIG3
157	40843_at1293	AF012023	7.44E-05	5.92E-05	1.02E-06	0.50623	ICAP-1A
158	1445_at1294	AF014958	2.11E-06	4.31E-06	1.05E-07	-0.42152	CCRL2
163	35450_s_at1295	AF015553	2.11E-06	9.54E-07	2.61E-07	0.61214	GTF2I
170	31675_s_at1296	AF019083	1.37E-05	5.01E-06	8.34E-07	0.17011	PTENP1
205	36100_at1297	AF022375	2.64E-07	8.23E-08	1.87E-11	-1.35847	VEGF
165	31410_at1298	AF023614	1.37E-05	1.51E-05	4.79E-07	-0.20744	TACI
166	1953_at1299	AF024710	8.55E-11	8.55E-11	1.13E-12	-1.95537	VEGF
171	38365_at1300	AF026086	0.0003443	4.67E-05	2.66E-06	0.297942	PEX1
193	38628_at1301	AF029777	1.37E-05	7.05E-06	8.27E-07	0.290159	GCN5L2
169	32756_at1302	AF030249	1.37E-05	1.61E-06	1.98E-07	0.534547	ECH1
172	37794_at1303	AF035281	2.11E-06	2.48E-06	4.87E-07	0.472445	
175	38349_at1304	AF038564	1.37E-05	1.61E-06	2.05E-07	-0.40446	ITCH
204	40498_g_at1305	AF040707	2.11E-06	1.99E-06	3.57E-07	0.289845	NPR2L
177	34962_at1306	AF042386	1.37E-05	5.01E-06	0.000107	0.137192	PPIE
200	3359	AF052160	7.44E-05	1.51E-05	1.67E-06	0.623021	

	8_r_at1307						
198	37842_at1308	AF054176	2.11E-06	1.33E-07	6.47E-09	-0.58138	C1orf7
203	40060_r_at1309	AF054589	0.0003443	2.35E-05	1.98E-06	0.945394	
189	36639_at1310	AF061258	7.44E-05	9.64E-05	1.58E-06	0.622201	LIM
190	40869_at1311	AF067853	1.37E-05	5.01E-06	5.02E-06	0.361707	ADSL
191	40870_g_at1312	AF069517	2.11E-06	1.33E-07	4.91E-07	0.399638	RBM6
201	351655_at1313	AF070582	2.64E-07	1.72E-07	3.23E-08	-0.19773	MGC13033
202	34188_at1314	AF070606	1.37E-05	3.06E-05	1.48E-06	-0.89337	
195	35142_at1315	AF070617	1.37E-05	3.86E-06	3.23E-07	0.323494	
208	41831_at1316	AF077820	2.64E-07	2.19E-08	2.91E-08	0.656852	LRP5
213	37233_at1317	AF079167	2.64E-07	2.49E-07	7.37E-10	-1.93249	OLR1
211	39430_at1318	AF082557	0.0013772	4.67E-05	2.23E-06	0.226994	TNKS
215	39562_at1319	AF094481	1.37E-05	5.01E-06	2.74E-07	-0.29045	CGGBP1
209	31472_s_at1320	AF098641	2.64E-07	1.72E-07	1.56E-07	-0.41172	
216	33810_at1321	AF110377	1.37E-05	5.01E-06	3.05E-05	0.361232	TRRAP
252	41384_at1322	AF117829	7.44E-05	0.000129	2.61E-06	-0.57516	RIPK2
275	35682_at1323	AI133727	7.44E-05	0.0001187	1.43E-06	0.181464	FLB6421
276	40175_at1324	AI141670	0.0003443	0.0003041	1.60E-06	-0.2494	CLCN2

277	40670_at~~325~~	AI148772	0.0003443	4.67E-05	4.18E-06	-1.02619	KYNU
278	37936_at~~326~~	AI184802	2.64E-07	2.19E-08	2.67E-09	-0.21576	HPRP4P
279	32021_at~~327~~	AI560890	2.57E-08	2.83E-08	1.80E-07	0.179028	
280	34724_at~~328~~	AI670100	7.44E-05	2.58E-05	7.70E-07	0.22677	GRLF1
281	39257_at~~329~~	AI754391	1.37E-05	3.86E-06	1.72E-06	-0.27657	KLF12
282	36484_at~~330~~	AI935146	0.0003443	2.35E-05	2.05E-06	-0.46726	GALNT3
283	35850_at~~331~~	AI950382	1.37E-05	1.61E-06	1.63E-07	-0.74128	KIAA0585
284	34751_at~~332~~	AI970189	0.0003443	2.35E-05	6.16E-07	-0.75934	KIAA0997
168	39392_at~~333~~	AJ002190	7.44E-05	1.61E-06	2.17E-08	0.33775	GNPAT
234	38988_at~~334~~	AJ007042	2.64E-07	1.72E-07	2.10E-07	0.170935	WHSC1
224	40723_at~~335~~	AJ010059	2.11E-06	5.05E-07	2.95E-06	0.2235	SIT
217	39561_at~~336~~	AL008583	2.64E-07	2.19E-08	1.12E-08	0.250082	CBX6
192	37043_at~~337~~	AL021154	0.0003443	4.67E-05	2.19E-06	-0.82935	ID3
222	34333_at~~338~~	AL021707	0.0003443	7.05E-06	4.95E-06	-2.21462	
199	40721_g_at~~1339~~	AL022398	7.44E-05	1.61E-06	8.09E-08	0.919627	
199	40720_at~~340~~	AL022398	7.44E-05	7.05E-06	1.10E-07	0.79713	DJ434O14.3
199	33734_at~~341~~	AL022398	7.44E-05	2.58E-05	2.40E-06	0.493166	
218	37189_at~~342~~	AL023553	1.37E-05	1.75E-05	2.51E-06	0.226635	PMM1

220	32672_at~~343~~	AL049387	0.0013772	0.0001897	5.12E-06	0.379296	
221	36021_at~~344~~	AL049409	7.44E-05	1.51E-05	1.10E-06	0.714173	LEF1
230	33687_at~~345~~	AL049782	7.44E-05	2.58E-05	7.66E-07	0.237794	
231	34239_at~~346~~	AL049787	1.37E-05	5.01E-06	7.11E-06	0.311278	
250	40456_at~~347~~	AL049963	0.0003443	4.67E-05	8.36E-07	-0.74421	LOC64116
226	41335_at~~348~~	AL050084	7.44E-05	1.61E-06	5.26E-05	0.509331	DC8
227	39976_at~~349~~	AL050087	2.11E-06	2.48E-06	1.27E-07	-0.31279	KIAA1785
228	38296_at~~350~~	AL050196	1.37E-05	5.01E-06	2.00E-05	-0.24688	DKFZP586D2223
229	31896_at~~351~~	AL050281	0.0003443	0.0002051	2.85E-06	0.30517	NAG
232	36968_s_at~~1352~~	AL050353	0.0003443	2.35E-05	4.42E-06	0.179352	OIP2
233	38090_at~~353~~	AL050371	0.0003443	2.35E-05	3.70E-06	0.493288	PISD
236	35715_at~~354~~	AL080071	0.0003443	0.0003041	3.12E-06	0.237367	DKFZP564M082
237	38859_at~~355~~	AL080141	1.37E-05	5.01E-06	2.42E-07	0.330868	SEC31B-1
238	32033_at~~356~~	AL096780	1.37E-05	5.05E-07	2.13E-06	0.34487	CHKL
285	33192_g_at~~1357~~	AW051579	1.37E-05	1.61E-06	7.58E-07	0.593476	FLJ10512
49	32567_at~~358~~	D10704	1.37E-05	1.75E-05	4.69E-07	-0.36791	CHK
74	41215_s_at~~1359~~	D13891	2.11E-06	2.48E-06	4.57E-05	-0.20577	ID2
75	3741	D30758	2.11E-06	1.99E-06	1.58E-05	0.27738	CENTB

	1_at~~1360~~						1
162	34476_rat~~1361~~	D30783	2.57E-08	2.83E-08	8.95E-10	-1.65011	EREG
107	38523_fat~~1362~~	D49677	7.44E-05	7.05E-06	4.18E-06	0.198707	U2AF1RS2
207	35234_at~~1363~~	D50406	1.37E-05	3.86E-06	2.65E-05	0.461907	RECK
110	33683_at~~1364~~	D50525	0.0003443	4.67E-05	3.02E-06	0.486698	
133	40662_g_at~~1365~~	D78579	1.37E-05	7.05E-06	4.25E-07	-1.65638	NR4A3
133	40661_at~~1366~~	D78579	7.44E-05	7.05E-06	9.62E-07	-1.61438	NR4A3
134	34034_at~~1367~~	D80011	7.44E-05	1.61E-06	4.20E-07	-0.35073	KIAA0189
127	40113_at~~1368~~	D87119	7.44E-05	2.35E-05	1.80E-06	0.425625	GS3955
127	717_at~~1369~~	D87119	7.44E-05	5.23E-05	4.62E-06	0.557116	GS3955
135	35039_at~~1370~~	D87466	1.37E-05	8.66E-06	1.49E-07	0.466046	KIAA0276
286	1877_g_at~~1371~~	HG1103-HT1103	1.37E-05	1.61E-06	1.16E-07	-0.39165	
287	1743_s_at~~1372~~	HG2007-HT2056	7.44E-05	9.64E-05	4.01E-06	-0.41408	
288	1842_at~~1373~~	HG2724-HT2820	1.37E-05	3.06E-05	5.17E-06	-1.33814	
289	1162_g_at~~1374~~	HG3227-HT3404	2.64E-07	1.72E-07	1.68E-08	-0.25361	
290	706_at~~1375~~	HG4582-HT4987	7.44E-05	2.35E-05	4.63E-07	-0.39588	
30	38029_at~~1376~~	J02939	7.44E-05	1.61E-06	2.16E-07	-0.87844	SLC3A2
63	33803_at~~1377~~	J02973	1.37E-05	5.05E-07	2.93E-07	-1.30804	THBD
66	1388	J03258	0.0003443	0.0001695	1.21E-06	-0.58295	VDR

		g_at 1378						
24		36674_at 379	J04130	0.0003443	2.35E-05	3.02E-06	-0.62071	SCYA4
58		39057_at 380	L04733	0.0013772	2.35E-05	8.84E-07	0.306455	KNS2
59		1125_s_at 1381	L05424	2.11E-06	1.33E-07	2.27E-09	-0.58081	CD44
99		2061_at 1382	L12002	7.44E-05	4.67E-05	1.23E-06	0.286717	ITGA4
55		280_g_at 383	L13740	2.64E-07	2.19E-08	5.83E-08	-1.45891	NR4A1
55		279_at 1384	L13740	1.37E-05	5.01E-06	9.10E-08	-0.61928	NR4A1
57		39037_at 385	L13773	1.37E-05	1.75E-05	6.44E-07	0.247919	MLLT2
54		37497_at 386	L16499	1.37E-05	8.66E-06	5.12E-06	0.374296	HHEX
79		33943_at 387	L20941	2.64E-07	1.33E-07	1.78E-06	-0.58618	FTH1
70		1139_at 1388	L22075	2.64E-07	2.49E-07	1.10E-08	-0.55736	GNA13
68		32372_at 389	L22569	1.37E-05	8.66E-06	1.52E-06	0.318129	CTSB
96		37903_at 390	L25665	0.0003443	0.0001695	3.34E-06	-0.4513	GNL1
90		1603_g_at 1391	L33881	2.64E-07	1.72E-07	5.06E-08	-0.59585	PRKCI
109		36312_at 392	L40377	1.37E-05	5.05E-07	3.49E-07	-0.79409	SERPINB8
105		37579_at 393	L47738	2.57E-08	4.01E-09	7.54E-09	0.31646	PIR121
148		1846_at 1394	L78132	7.44E-05	5.23E-05	5.15E-07	0.358576	LGALS8
46		36636_at 395	M12267	0.0003443	0.0001695	4.07E-06	-0.3279	OAT
60		1106_s_at	M12959	7.44E-05	2.58E-05	1.61E-06	0.128482	TRA@

		1396						
39		39402_at1397	M15330	8.55E-11	8.55E-11	2.49E-12	-2.13825	IL1B
25		35372_r_at1398	M17017	7.44E-05	0.0001187	1.43E-06	-1.74073	IL8
44		33993_at1399	M22919	2.64E-07	3.12E-07	9.52E-08	-0.81053	MYL6
35		39791_at1400	M23114	2.11E-06	4.31E-06	1.59E-07	-0.96141	ATP2A2
43		34609_g_at1401	M24194	7.44E-05	1.61E-06	4.38E-06	0.560895	GNB2L1
36		32640_at1402	M24283	0.0003443	4.67E-05	3.71E-06	-1.32611	ICAM1
85		36680_at1403	M24895	2.11E-06	1.33E-07	1.72E-08	0.476779	AMY2B
37		875_g_at1404	M26683	7.44E-05	0.0001187	3.70E-06	-0.16179	SCYA2
40		1368_at1405	M27492	0.0003443	0.0004017	2.01E-06	-0.32619	IL1R1
41		1369_s_at1406	M28130	7.44E-05	4.67E-05	8.02E-07	-2.27292	IL8
64		1372_at1407	M31165	7.44E-05	5.23E-05	1.38E-06	-0.34617	TNFAIP6
61		1373_at1408	M31523	1.37E-05	1.75E-05	2.09E-06	0.36898	TCF3
33		34022_at1409	M36821	1.37E-05	8.66E-06	2.21E-07	-0.36334	GRO3
62		38404_at1410	M55153	7.44E-05	2.58E-05	4.77E-06	-0.27465	TGM2
45		1378_g_at1411	M58603	7.44E-05	5.23E-05	1.28E-06	-0.73537	NFKB1
26		2036_s_at1412	M59040	0.0013772	2.35E-05	2.82E-06	-0.46271	CD44
65		40842_at1413	M60784	7.44E-05	5.23E-05	1.24E-06	0.559903	SNRPA
95		32181_at1	M60922	7.44E-05	1.51E-05	4.47E-08	0.39657	FLOT2

		414						
38		1737_s_at1415	M62403	7.44E-05	5.23E-05	5.57E-07	-0.53749	IGFBP4
27		36190_at1416	M63256	0.0003443	5.92E-05	6.54E-07	0.454561	CDR2
31		40365_at1417	M63904	2.57E-08	1.03E-08	5.38E-09	-0.59612	GNA15
67		36101_s_at1418	M63978	0.0003443	4.67E-05	1.77E-06	-0.44762	VEGF
42		242_at1419	M64571	1.84E-09	1.84E-09	2.41E-11	0.416659	MAP4
91		38326_at1420	M69199	2.11E-06	1.99E-06	1.45E-07	-1.9021	G0S2
48		1252_at1421	M73547	1.37E-05	5.01E-06	9.20E-08	0.438897	D5S346
34		1231_at1422	M74525	2.11E-06	2.48E-06	3.50E-07	-0.61792	UBE2B
28		32186_at1423	M80244	0.0003443	7.05E-06	2.72E-06	-0.8522	SLC7A5
32		37825_at1424	M84443	1.37E-05	5.05E-07	4.08E-07	0.303567	GALK2
29		39799_at1425	M94856	7.44E-05	5.23E-05	4.99E-06	-0.23847	FABP5
47		210_at1426	M95678	0.0003443	7.05E-06	2.00E-06	0.432923	PLCB2
241		41425_at1427	M98833	7.44E-05	1.61E-06	1.52E-06	0.434288	FLI1
261		35969_at1428	N23137	2.11E-06	2.48E-06	2.06E-07	0.247311	MPHOSPH9
261		35970_g_at1429	N23137	0.0013772	0.0001695	4.12E-06	0.244083	MPHOSPH9
262		40885_s_at1430	N30151	7.44E-05	1.61E-06	5.05E-05	0.393521	STX16
263		40564_at1431	N42007	2.11E-06	2.48E-06	9.19E-05	0.167986	NUP50

264	39693_at1432	N53547	7.44E-05	8.56E-05	1.80E-07	0.296678	MGC5508
269	32715_at1433	N90862	1.37E-05	5.05E-07	3.28E-08	0.43576	VAMP8
270	34210_at1434	N90866	2.64E-07	8.23E-08	2.76E-08	0.304525	CDW52
265	39551_at1435	N98667	1.37E-05	8.66E-06	3.38E-07	0.367127	KIAA1696
260	34779_at1436	R90942	1.37E-05	5.01E-06	1.05E-05	-0.17696	ST6GALNACIV
53	32962_at1437	S52028	2.11E-06	5.05E-07	9.62E-08	-0.81662	CTH
87	32066_g_at1438	S68134	0.0003443	7.05E-06	8.37E-07	-1.64652	CREM
87	32065_at1439	S68134	0.0003443	7.05E-06	4.35E-06	-2.47105	CREM
86	32067_at1440	S68271	0.0003443	7.05E-06	3.03E-06	-2.07185	CREM
92	31508_at1441	S73591	1.37E-05	1.51E-05	4.68E-06	0.414777	VDUP1
50	545_g_at1442	S76638	7.44E-05	2.35E-05	7.47E-07	-0.35416	NFKB2
51	1347_at1443	S78187	7.44E-05	1.61E-06	1.95E-05	0.203265	CDC25B
52	36209_at1444	S78771	0.0003443	5.92E-05	2.55E-06	-0.31389	BRD2
126	1237_at1445	S81914	0.0003443	7.05E-06	4.18E-07	-1.59146	IER3
69	33849_at1446	U02020	1.37E-05	8.66E-06	1.37E-06	-1.13863	PBEF
71	553_g_at1447	U02570	1.37E-05	2.81E-05	1.26E-06	0.432431	ARHGAP1
73	554_at1448	U03634	1.37E-05	1.75E-05	1.00E-06	-0.21467	LBC
76	1069_at1449	U04636	0.0003443	5.92E-05	2.81E-06	-1.85123	PTGS2

83	1796_s_at1450	U05681	7.44E-05	5.23E-05	3.37E-06	-0.35383	BCL3
81	1635_at1451	U07563	7.44E-05	2.35E-05	4.91E-07	-0.25016	ABL1
82	189_s_at1452	U09937	1.84E-09	4.16E-10	2.04E-09	-1.21578	PLAUR
77	39734_at1453	U10117	7.44E-05	1.51E-05	4.07E-06	0.563673	SCYE1
80	38491_at1454	U11732	1.37E-05	3.86E-06	3.04E-07	-0.22574	ETV6
101	40659_at1455	U12767	7.44E-05	1.61E-06	2.84E-07	-1.23483	NR4A3
101	190_at1456	U12767	0.0003443	7.05E-06	2.55E-07	-2.13744	NR4A3
84	525_g_at1457	U13695	7.44E-05	1.61E-06	1.11E-05	0.805607	PMS1
88	37938_at1458	U15552	1.37E-05	5.01E-06	1.67E-05	-0.68094	HSU15552
94	36929_at1459	U17760	0.0003443	7.05E-06	4.25E-06	-0.84472	LAMB3
131	1243_at1460	U18300	7.44E-05	0.000129	2.43E-06	0.183171	DDB2
93	39781_at1461	U20982	2.11E-06	1.99E-06	1.20E-08	-0.67125	IGFBP4
104	33456_at1462	U24166	7.44E-05	1.61E-06	7.52E-06	-0.45293	MAPRE1
121	37706_at1463	U28811	0.0003443	7.05E-06	1.33E-06	0.32855	GLG1
97	493_at1464	U29171	1.37E-05	5.01E-06	1.10E-06	-0.6032	CSNK1D
98	32579_at1465	U29175	1.37E-05	8.66E-06	1.90E-06	0.266342	SMARCA4
181	36159_s_at1466	U29185	2.11E-06	7.73E-07	1.56E-07	-1.08006	PRNP
100	38429_at1467	U29344	2.11E-06	9.54E-07	2.35E-07	-0.43842	FASN

106	198_g_at~~1468~~	U29656	2.11E-06	7.73E-07	7.52E-08	0.353186	NME3
106	197_at~~14699~~	U29656	7.44E-05	0.000129	4.31E-06	0.471876	NME3
102	496_s_at~~1470~~	U32324	1.37E-05	5.05E-07	3.21E-08	0.334966	IL11RA
103	33513_at~~1471~~	U33017	2.64E-07	1.72E-07	5.20E-07	0.373581	SLAM
112	39779_at~~1472~~	U38847	7.44E-05	2.35E-05	9.91E-07	0.222946	TARBP1
111	38911_at~~1473~~	U41815	1.37E-05	5.05E-07	2.16E-07	-0.96931	NUP98
124	38868_at~~1474~~	U43774	0.0003443	2.35E-05	8.80E-07	-0.39938	FCAR
118	162_at~~14755~~	U44839	2.11E-06	9.54E-07	2.54E-07	-0.97008	USP11
120	37723_at~~1476~~	U47414	2.11E-06	9.54E-07	2.31E-06	0.370736	CCNG2
113	34405_at~~1477~~	U47927	2.57E-08	2.83E-08	5.53E-09	0.545592	USP5
115	1788_s_at~~1478~~	U48807	1.37E-05	5.01E-06	4.97E-08	-0.93178	DUSP4
119	32977_at~~1479~~	U49187	7.44E-05	1.51E-05	1.48E-06	0.671467	C6orf32
119	32978_g_at~~14800~~	U49187	7.44E-05	9.64E-05	3.53E-06	0.511392	C6orf32
114	37229_at~~1481~~	U49844	7.44E-05	7.05E-06	3.67E-07	0.47168	ATR
130	1527_s_at~~1482~~	U50527	1.37E-05	5.01E-06	5.11E-06	0.416543	
122	38120_at~~1483~~	U50928	7.44E-05	1.61E-06	4.72E-06	0.302213	PKD2
116	39749_at~~1484~~	U51007	7.44E-05	1.51E-05	1.49E-06	0.309996	PSMD4
138	32539_at~~1485~~	U51205	1.37E-05	5.05E-07	2.65E-07	-0.76279	COP9

129	32563_at~~1~~ ~~486~~	U51478	7.44E-05	2.35E-05	6.10E-07	-0.58	ATP1B3
117	36060_at~~1~~ ~~487~~	U51920	2.11E-06	1.33E-07	7.01E-08	-0.28142	SRP54
128	34356_at~~1~~ ~~488~~	U52960	2.11E-06	1.61E-06	1.51E-07	-0.84863	SURB7
125	806_at~~1489~~	U56998	0.0003443	7.05E-06	3.70E-06	-0.74294	CNK
141	40385_at~~1~~ ~~490~~	U64197	1.84E-09	1.84E-09	2.95E-10	-0.62373	SCYA20
132	1789_at~~14~~ ~~91~~	U65928	7.44E-05	4.67E-05	2.85E-07	0.408918	COPS5
164	32105_f_at~~1492~~	U66063	2.11E-06	2.48E-06	4.70E-07	0.277185	CAMK2G
161	40138_at~~1~~ ~~493~~	U70735	1.37E-05	8.66E-06	1.82E-06	0.249185	MOV34-34KD
139	35227_at~~1~~ ~~494~~	U72066	2.57E-08	1.03E-08	4.33E-08	-0.34482	RBBP8
136	31935_s_at~~1495~~	U75968	2.11E-06	1.99E-06	4.36E-06	0.139542	DDX11
137	40289_at~~1~~ ~~496~~	U78107	8.55E-11	3.69E-11	4.04E-12	-0.43769	NAPG
174	38104_at~~1~~ ~~497~~	U78302	2.64E-07	1.72E-07	2.41E-08	0.329878	DECR1
140	1209_at~~14~~ ~~98~~	U78798	2.57E-08	4.01E-09	1.11E-06	-0.3172	TRAF6
142	38252_s_at~~1499~~	U84007	7.44E-05	1.61E-06	0.000235	0.236422	AGL
143	35741_at~~1~~ ~~500~~	U85245	7.44E-05	1.61E-06	4.57E-07	0.365266	PIP5K2B
150	40606_at~~1~~ ~~501~~	U88629	0.0003443	4.67E-05	9.58E-07	-0.32607	ELL2
147	41323_at~~1~~ ~~502~~	U90917	1.37E-05	1.61E-06	3.89E-07	0.433406	FOXM1
196	34707_at~~1~~	U91543	2.64E-07	3.12E-07	2.01E-07	0.478678	CHD3

		503						
149		38276_at 504	U91616	1.37E-05	5.05E-07	1.27E-07	-0.80419	NFKBIE
160		35303_at 505	U96876	7.44E-05	1.61E-06	3.54E-06	-0.45317	INSIG1
185		40607_at 506	U97105	1.37E-05	1.75E-05	6.56E-07	1.00615	DPYSL2
266		39296_at 507	W28319	1.37E-05	5.01E-06	1.50E-05	0.294631	FBLN1
267		33328_at 508	W28612	1.37E-05	5.01E-06	1.70E-06	-0.25519	
268		36856_at 509	W28743	0.0003443	7.05E-06	2.78E-06	-0.28926	PP1628
18		430_at 1510	X00737	2.11E-06	9.54E-07	5.21E-08	-0.67074	NP
12		41485_at 511	X02152	1.37E-05	5.05E-07	4.63E-08	-0.75601	LDHA
4		33908_at 512	X04366	1.37E-05	2.81E-05	5.11E-06	0.346076	CAPN1
10		1520_s_at 1513	X04500	2.64E-07	1.72E-07	3.43E-10	-2.12121	IL1B
6		39753_at 514	X06256	1.37E-05	2.35E-05	4.89E-07	-0.7357	ITGA5
16		40896_at 515	X13403	7.44E-05	5.92E-05	4.21E-07	0.146032	POU2F1
21		1866_g_at 1516	X15217	7.44E-05	4.67E-05	3.77E-07	-0.2371	SKIL
20		41499_at 517	X15218	8.55E-11	8.55E-11	1.40E-10	-1.41501	SKI
14		40074_at 518	X16396	0.0003443	0.0002051	3.27E-06	-0.6151	MTHFD2
7		40268_at 519	X16706	7.44E-05	1.61E-06	1.23E-06	-1.09747	FOSL2
11		41266_at 520	X53586	1.37E-05	8.66E-06	3.40E-07	0.51291	ITGA6
1		32145_at 521	X58141	7.44E-05	9.64E-05	1.75E-06	0.384254	ADD1

3	37294_at~~522~~	X61123	7.44E-05	0.0001057	4.17E-07	-1.15256	BTG1
13	40362_at~~523~~	X61498	7.44E-05	1.61E-06	8.80E-07	-0.49884	NFKB2
5	32716_at~~524~~	X62535	1.37E-05	1.61E-06	5.68E-07	0.243937	DGKA
249	37365_at~~525~~	X63368	2.11E-06	5.05E-07	2.30E-08	-0.55432	DNAJB2
2	40881_at~~526~~	X64330	7.44E-05	7.05E-06	2.27E-06	0.297851	ACLY
22	39183_at~~527~~	X66363	2.64E-07	1.72E-07	6.53E-07	-0.24505	PCTK1
9	37904_s_at~~1528~~	X66436	0.0003443	8.56E-05	1.88E-06	-0.26662	
15	424_s_at~~529~~	X66945	7.44E-05	1.51E-05	1.91E-07	-0.35494	FGFR1
23	1983_at~~1530~~	X68452	2.57E-08	4.01E-09	9.12E-11	-0.26618	CCND2
19	32444_at~~531~~	X69392	2.64E-07	1.33E-07	1.10E-08	0.297444	RPL26
212	382_at~~1532~~	X70218	1.37E-05	3.06E-05	2.44E-06	-0.74691	PPP4C
72	41169_at~~533~~	X74039	1.84E-09	4.16E-10	1.51E-10	-0.67381	PLAUR
242	38064_at~~534~~	X79882	1.37E-05	5.05E-07	1.78E-07	0.520965	MVP
89	38466_at~~535~~	X82153	7.44E-05	1.61E-06	2.27E-06	0.47844	CTSK
253	37283_at~~536~~	X82209	2.11E-06	5.05E-07	1.37E-09	-0.45281	MN1
108	36614_at~~537~~	X87949	7.44E-05	1.61E-06	4.05E-07	-0.54468	HSPA5
123	33774_at~~538~~	X98172	7.44E-05	4.67E-05	5.29E-07	0.507556	CASP8
146	32329_at~~539~~	X99142	1.37E-05	8.66E-06	1.24E-06	-0.29773	KRTHB6

144	39159_at~~1540~~	X99656	1.37E-05	5.05E-07	1.68E-06	-0.23553	SH3GL1
17	37185_at~~1541~~	Y00630	2.57E-08	3.70E-08	6.65E-09	-2.38485	SERPINB2
145	35936_g_at~~1542~~	Y08683	1.37E-05	5.05E-07	4.71E-06	0.492738	CPT1B
206	40729_s_at~~1543~~	Y14768	1.37E-05	5.05E-07	7.26E-08	0.248383	LTB
219	38518_at~~1544~~	Y18004	1.37E-05	5.01E-06	4.19E-07	-0.9465	SCML2
8	37536_at~~1545~~	Z11697	1.37E-05	5.05E-07	3.55E-06	-1.21033	CD83
56	35685_at~~1546~~	Z14000	0.0003443	0.0002051	3.91E-06	-0.33734	RING1
78	34857_at~~1547~~	Z24724	2.64E-07	2.19E-08	5.96E-09	-1.10426	
259	33588_at~~1548~~	Z32860	1.37E-05	5.01E-06	7.81E-06	0.133192	
225	39756_g_at~~1549~~	Z93930	2.64E-07	2.49E-07	2.42E-05	-0.39839	XBP1

Table III: Differential Gene Expression in acute MS relapse vs. remission

Affymetrix ID no:~~SEQ ID NO:~~	Identifier	TNOM PValue	Info PValue	t-Test PValue	Log Fold Change	Symbol
38592_s_at~~1550~~	AI828210	5.38E-06	5.38E-06	8.37E-06	-0.18947	KIAA0284
40096_at~~1551~~	D14710	6.73E-05	3.19E-05	2.89E-05	-0.35496	ATP5A1
35816_at~~1~~	U46692	6.73E-05	3.19E-05	0.000284	-0.49741	CSTB

552						
33318_at553	AF061261	6.73E-05	3.19E-05	3.22E-05	-0.28274	MBLL
39698_at554	U51712	6.73E-05	3.19E-05	0.003464	-0.42775	SMAP31
35852_at555	AB014558	6.73E-05	4.25E-05	0.000473	0.694784	CRY2
41458_at556	AB007936	6.73E-05	4.25E-05	0.000958	-0.25409	KIAA0467
34880_at557	AC002115	6.73E-05	4.25E-05	0.000147	0.622841	MGC10433
34962_at558	AF052160	6.73E-05	4.25E-05	0.000182	-0.46468	
855_at1559	S78085	0.000538	0.000104	0.000102	-0.55064	PDCD2
38839_at560	AL096719	0.000538	0.000104	0.000089	-0.22287	PFN2
36176_at561	U61234	0.000538	0.000104	0.000844	0.299182	TBCC
37391_at562	X12451	0.000538	0.000251	0.000876	1.04444	CTSL
40337_at563	M35531	0.000538	0.000251	0.000241	-0.20303	FUT1
1457_at1564	M64174	0.000538	0.000251	3.43E-05	-0.5508	JAK1
41423_at565	AB018269	0.000538	0.000251	7.39E-05	-0.18186	KIAA0726
36130_f_at1566	R92331	0.000538	0.000251	0.000104	0.289994	MT1E
828_at1567	U19487	0.000538	0.000251	0.001738	-0.25888	PTGER2
39847_at568	AF040965	0.000538	0.000251	0.000775	0.48898	RES4-25
32974_at569	U07563	0.000538	0.000251	3.61E-05	-0.16779	RRP4
36312_at	L40377	0.000538	0.000251	0.009479	0.452416	SERPINB8

570						
38070_at571	AL080234	0.000538	0.000251	0.000377	-0.52631	
35479_at572	AJ242015	0.003096	0.00039	0.013957	0.281618	ADAM28
39317_at573	D86324	0.003096	0.00039	0.001801	-0.34728	CMAH
33195_at574	M94065	0.003096	0.00039	0.002391	-0.13976	DHODH
34810_at575	AC004382	0.003096	0.00039	0.000121	-0.20383	DKFZP434K046
35300_at576	X54326	0.003096	0.00039	0.002734	-0.39559	EPRS
40433_at577	W25921	0.003096	0.00039	9.41E-05	-0.39027	GNS
35010_at578	X92110	0.003096	0.00039	0.000103	-1.00581	HCGVIII-1
40913_at579	W28589	0.003096	0.00039	0.000225	-0.20949	HSPD1
33411_g_at1580	S66213	0.003096	0.00039	0.000134	-0.28606	ITGA6
37232_at581	AB011158	0.000538	0.00039	0.000047	-0.163	KIAA0586
41191_at582	AB023209	0.003096	0.00039	0.003354	-0.09151	KIAA0992
40036_at583	AF035940	0.003096	0.00039	0.008457	0.282437	MAGOH
588_at1584	M31724	0.003096	0.00039	0.000671	0.569343	PTPN1
1318_at1585	X74262	0.003096	0.00039	0.000062	-0.37623	RBBP4
1119_at1586	J05249	0.003096	0.00039	0.00045	-0.52346	RPA2
34362_at587	M55531	0.003096	0.00039	0.023054	-0.22329	SLC2A5
35149_at	AI865431	0.003096	0.00039	0.00027	0.423067	TNFRSF5

588						
31372_at589	W28203	0.003096	0.00039	0.007983	-0.17484	
34036_at590	W28667	0.003096	0.00039	0.000846	-0.49488	
39315_at591	D13628	0.000538	0.000529	0.034335	-0.10398	ANGPT1
37012_at592	U03271	0.000538	0.000529	0.000286	-0.1675	CAPZB
38017_at593	U05259	0.000538	0.000529	0.003589	0.551328	CD79A
37902_at594	L13278	0.000538	0.000529	7.27E-05	-0.43636	CRYZ
40619_at595	M91670	0.000538	0.000529	0.003472	0.600255	E2-EPF
38961_at596	AB029030	0.000538	0.000529	0.000657	-0.13458	KIAA1107
41304_at597	AF016098	0.000538	0.000529	0.000433	-0.16189	NRP2
35047_at598	X76091	0.000538	0.000529	0.004691	0.161349	RFX2
37583_at599	U52191	0.000538	0.000529	0.00229	1.2356	SMCY
41121_at600	AA203345	0.000538	0.000529	0.001228	-0.50409	STX16
784_g_at601	U96113	0.000538	0.000529	0.000394	-0.41425	WWP1
31656_at602	AL050263	0.000538	0.000529	0.000224	-0.15981	
40798_s_at1603	Z48579	0.000538	0.000799	0.000184	-0.30836	ADAM10
41109_at604	M31452	0.000538	0.000799	0.002899	-0.13022	C4BPA
40162_s_at1605	AC003107	0.000538	0.000799	0.000262	-0.16818	COMP
893_	M91670	0.000538	0.000799	0.000792	0.41925	E2-EPF

at1606						
36458_at1607	AB023235	0.000538	0.000799	0.001348	-0.30138	KIAA1018
37436_at1608	X89960	0.000538	0.000799	0.026837	-0.35169	MCSP
36608_at1609	D55654	0.000538	0.000799	0.019331	-0.2254	MDH1
38569_at1610	U02683	0.000538	0.000799	0.030035	-0.09324	NRF1
858_at1611	S90469	0.000538	0.000799	0.000785	0.23032	POR
38108_at1612	AF020543	0.000538	0.000799	0.004286	-0.25061	PPT2
36215_at1613	M34181	0.000538	0.000799	0.000055	-0.5883	PRKACB
33730_at1614	AF095448	0.000538	0.000799	0.000588	-0.24961	RAI3
41363_at1615	AF027150	0.000538	0.000799	0.000979	-0.16012	SIP1
33678_i_at1616	X02344	0.000538	0.000799	0.000918	0.430531	TUBB2
33679_f_at1617	X02344	0.000538	0.000799	0.002225	0.296682	TUBB2
37662_at1618	AI701164	0.000538	0.000799	0.000115	-0.23639	UBE2G1
783_at1619	U96113	0.000538	0.000799	9.77E-05	-0.45711	WWP1
33306_at1620	AF016052	0.000538	0.000799	0.001254	-0.19092	ZNF24
38201_at1621	U21551	0.003096	0.00103	0.000836	0.278219	BCAT1
1920_s_at1622	X77794	0.003096	0.00103	3.72E-05	-0.81938	CCNG1
35230_at1623	AF070530	0.003096	0.00103	0.014908	0.276942	CL24751

32045_at1624	AB002331	0.003096	0.00103	0.001714	-0.17304	DATF1
36732_at1625	AI004207	0.003096	0.00103	0.000762	-0.1648	FLJ00002
905_at1626	L76200	0.003096	0.00103	0.000824	0.444479	GUK1
33508_at1627	U26398	0.003096	0.00103	0.001182	-0.29185	INPP4A
38203_at1628	U69883	0.003096	0.00103	0.007922	0.103614	KCNN1
37377_i_at1629	M13452	0.003096	0.00103	0.000467	0.405856	LMNA
41289_at1630	AA126505	0.003096	0.00103	0.002	-0.39781	NCAM1
38335_at1631	U88620	0.003096	0.00103	0.007562	-0.3532	OGG1
227_g_at1632	M33336	0.003096	0.00103	0.001568	-0.26454	PRKAR1A
37876_at1633	AB015982	0.003096	0.00103	0.000382	-0.27486	PRKCN
41446_f_at1634	H68340	0.003096	0.00103	0.001222	0.516352	RNAHP
34375_at1635	M28225	0.003096	0.00103	0.000686	1.0733	SCYA2
39099_at1636	X97064	0.003096	0.00103	0.003207	-0.19906	SEC23A
41573_at1637	X68560	0.003096	0.00103	0.007856	0.437567	SP3
37789_at1638	AF064094	0.003096	0.00103	0.000287	-0.19385	TADA2L
41612_at1639	AB007872	0.003096	0.00103	0.000119	-0.20778	ZNF264
40984_at1640	W28255	0.013622	0.001698	0.001407	-0.24426	76P
38704_at1	AB007934	0.003096	0.001698	0.003182	-0.24405	ACF7

641						
34792_at642	AL049954	0.013622	0.001698	0.024193	-0.25818	AHCYL1
38760_f_at1643	U90546	0.003096	0.001698	0.000105	-0.34074	BTN3A2
38712_at644	AL035291	0.013622	0.001698	0.007668	0.506107	CH1
35349_at645	AF031647	0.013622	0.001698	0.004755	0.257244	COPS3
32370_at646	M57888	0.003096	0.001698	0.004549	-0.64384	CTLA1
40097_at647	AF000987	0.003096	0.001698	0.009455	0.247586	EIF1AY
40250_at648	U55766	0.003096	0.001698	0.00066	0.795017	HRB2
2061_at1649	L12002	0.013622	0.001698	0.005765	-0.1942	ITGA4
41635_at650	D14661	0.013622	0.001698	0.011324	0.391267	KIAA0105
40844_at651	D63875	0.013622	0.001698	0.002192	-0.36411	KIAA0155
34786_at652	AB018285	0.013622	0.001698	0.001545	0.550994	KIAA0742
37216_at653	AB023180	0.013622	0.001698	0.001642	0.253479	KIAA0963
32171_at654	AL080102	0.013622	0.001698	0.003651	0.435751	KIAA1856
39971_at655	M22637	0.013622	0.001698	0.003792	-0.27794	LYL1
1764_s_at1656	D85131	0.013622	0.001698	0.005126	-0.12291	MAZ
1761_at1657	D37965	0.013622	0.001698	0.01111	-0.09143	PDGFRL
39364_s_at1658	Y18207	0.003096	0.001698	0.003474	-0.17238	PPP1R3C
1571	L49229	0.013622	0.001698	0.000336	-0.36639	RB1

f_at 1659						
41040_at 660	U77664	0.013622	0.001698	0.002354	0.193666	RPP38
41807_at 661	AL040137	0.003096	0.001698	0.008384	-0.23366	SAP18
37654_at 662	D31764	0.013622	0.001698	0.01295	-0.13299	SNX17
41071_at 663	X57655	0.013622	0.001698	0.002476	-0.17382	SPINK2
36790_at 664	M19267	0.013622	0.001698	0.013582	0.262886	TPM1
1106_s_at 1665	M12959	0.013622	0.001698	0.003907	-0.08942	TRA@
33844_at 666	AA160724	0.013622	0.001698	0.005695	0.267002	
33103_s_at 1667	U37122	0.003096	0.002135	0.000571	-0.59281	ADD3
38554_at 668	AA903720	0.003096	0.002135	0.002557	0.244618	BAP29
37211_at 669	M93107	0.003096	0.002135	0.00187	-0.19146	BDH
41694_at 670	M17754	0.003096	0.002135	0.010333	-0.10769	BN51T
34802_at 671	X15882	0.003096	0.002135	0.0023	0.227769	COL6A2
38413_at 672	D15057	0.003096	0.002135	0.002814	-0.26776	DAD1
39420_at 673	S62138	0.003096	0.002135	0.002442	1.1158	DDIT3
38555_at 674	AB026436	0.003096	0.002135	0.011189	0.711919	DUSP10
38226_at 675	W27152	0.003096	0.002135	0.009498	-0.1614	FLJ10569
763_at 1676	AB001106	0.003096	0.002135	0.002408	0.444617	GMFB
3432	D87120	0.003096	0.002135	0.00475	0.236706	GS3786

2_r_at1677						
34157_f_at1678	AI200373	0.003096	0.002135	0.003822	-0.31066	H2AFI
41609_at1679	U15085	0.003096	0.002135	0.011743	0.328857	HLA-DMB
35737_at1680	U90549	0.003096	0.002135	0.001654	-0.26437	HMG17L3
41058_g_at1681	AI760162	0.003096	0.002135	0.001313	-0.47775	HT012
34832_s_at1682	AB018306	0.003096	0.002135	0.000371	0.316202	KIAA0763
39019_at1683	D14696	0.003096	0.002135	0.016949	0.259239	LAPTM4A
33238_at1684	U23852	0.003096	0.002135	0.001207	-0.2593	LCK
40138_at1685	U70735	0.003096	0.002135	0.0002	-0.20846	MOV34-34KD
39812_at1686	X79865	0.003096	0.002135	0.0141	0.418466	MRPL12
39081_at1687	AI547258	0.003096	0.002135	0.001223	0.267951	MT2A
269_at1688	L40387	0.003096	0.002135	0.00038	0.211973	OASL
34376_at1689	AB019517	0.003096	0.002135	0.023004	0.219453	PKIG
41214_at1690	M58459	0.003096	0.002135	0.001362	1.46854	RPS4Y
33322_i_at1691	X57348	0.003096	0.002135	0.004255	0.22047	SFN
32767_at1692	M74558	0.003096	0.002135	0.001205	0.219185	SIL
39387_at1693	U34044	0.003096	0.002135	0.000831	-0.21289	SPS

35634_at694	U49928	0.003096	0.002135	0.000886	-0.31189	TAB1
1634_s_at1695	X05839	0.003096	0.002135	0.008747	0.214552	TGFB1
37460_at696	U16296	0.003096	0.002135	0.006585	-0.14857	TIAM1
41443_at697	U63127	0.003096	0.002135	0.000538	-0.38925	TIC
31540_at698	U03397	0.003096	0.002135	0.005156	-0.34157	TNFRSF9
1110_at1699	M21624	0.003096	0.002135	0.001748	-0.51878	TRD@
36170_at700	D83198	0.003096	0.002135	0.028975	-0.17519	YF13H12
303_at1701	HG960-HT960	0.003096	0.002135	0.003089	0.145701	
918_at1702	HG4724-HT5166	0.003096	0.002135	0.002446	-0.25728	
1197_at1703	D00654	0.003096	0.004342	9.79E-05	-0.1819	ACTG2
40789_at704	U54645	0.013622	0.004342	0.004228	-0.25281	AK2
32676_at705	M93405	0.003096	0.004342	0.020651	0.126156	ALDH6A1
33796_at706	U73960	0.003096	0.004342	0.002279	0.555806	ARL4
2000_at1707	U26455	0.003096	0.004342	0.006562	-0.53911	ATM
33838_at708	M33519	0.003096	0.004342	0.011169	-0.33327	BAT3
40548_at709	U90028	0.003096	0.004342	0.000396	-0.24971	BICD1
37112_at710	AB002384	0.003096	0.004342	0.002855	-0.46941	C6orf32
41060_at711	M74093	0.003096	0.004342	0.000763	-0.33022	CCNE1
4182	AA203246	0.003096	0.004342	0.007014	-0.16607	CDC2L5

1_at712						
795_s_at713	X66358	0.013622	0.004342	0.007122	-0.1886	CDKL1
37302_at714	U30872	0.003096	0.004342	0.001715	-0.164	CENPF
37155_at715	AB020675	0.013622	0.004342	0.002913	-0.25056	CNTNAP2
1400_at1716	M13207	0.013622	0.004342	0.01388	0.122241	CSF2
34340_at717	AA173896	0.013622	0.004342	0.008401	0.305133	CYB5-M
35490_at718	L78267	0.003096	0.004342	0.04708	0.103949	D15S226E
36078_at719	AL080120	0.013622	0.004342	0.001834	-0.12922	DKFZP564O0423
40065_s_at1720	U13896	0.013622	0.004342	0.020482	-0.10291	DLG1
31514_at721	AF034970	0.013622	0.004342	0.010371	-0.10568	DOK2
1306_at1722	D12686	0.013622	0.004342	0.003493	0.170378	EIF4G1
32259_at723	AB002386	0.003096	0.004342	0.000131	-0.39255	EZH1
34960_g_at1724	M15059	0.003096	0.004342	0.002497	0.2061	FCER2
38362_at725	W27545	0.013622	0.004342	0.004445	0.379682	FLJ20259
37825_at726	M84443	0.003096	0.004342	0.000101	-0.27085	GALK2
38628_at727	AF029777	0.013622	0.004342	0.001427	-0.22426	GCN5L2
37959_at728	D63876	0.013622	0.004342	0.002737	0.396946	GGA3
34719_at729	AB020645	0.003096	0.004342	0.003907	-0.37377	GLS

466_at1730	U77948	0.003096	0.004342	0.000818	-0.35677	GTF2I
40778_at1731	AF035555	0.003096	0.004342	0.018388	-0.17666	HADH2
39733_at1732	AF055001	0.003096	0.004342	0.010744	0.724714	HERPUD1
41237_at1733	D32129	0.003096	0.004342	0.005364	-0.13287	HLA-A
31460_f_at1734	AF043586	0.003096	0.004342	0.001047	-0.30021	IGL@
36412_s_at1735	U53831	0.013622	0.004342	0.01853	0.488267	IRF7
41387_r_at1736	AB002344	0.003096	0.004342	0.001658	0.705775	KIAA0346
40222_s_at1737	AI677689	0.013622	0.004342	0.004375	-0.1411	KIAA0685
41431_at1738	AB023153	0.003096	0.004342	0.04282	-0.39134	KIAA0936
38919_at1739	AB023226	0.003096	0.004342	0.000111	-0.71413	KIAA1009
40670_at1740	AI148772	0.013622	0.004342	0.03739	0.532454	KYNU
35367_at1741	AB006780	0.003096	0.004342	0.010236	0.178362	LGALS3
36527_at1742	AL050405	0.003096	0.004342	0.008144	0.311843	LOC51634
1671_s_at1743	L35253	0.013622	0.004342	0.001324	-0.46397	MAPK14
39594_f_at1744	R93527	0.013622	0.004342	0.000372	0.264207	MT1H
41637_at1745	AF108145	0.003096	0.004342	0.001206	-0.14877	MYLE
32188_at1746	M96980	0.013622	0.004342	0.002106	-0.16409	MYT1

545_g_at747	S76638	0.013622	0.004342	0.04529	0.171344	NFKB2
33367_s_at1748	D88674	0.013622	0.004342	0.045232	0.346415	OAZIN
36968_s_at1749	AL050353	0.013622	0.004342	0.016071	-0.11979	OIP2
40440_at750	AL080119	0.003096	0.004342	0.001961	-0.40821	PAI-RBP1
34855_at751	X76770	0.013622	0.004342	0.005011	-0.10613	PAPOLA
39993_at752	D11466	0.003096	0.004342	0.009752	0.738127	PIGA
35361_at753	W28299	0.003096	0.004342	0.001225	-0.17755	PINK1
37028_at754	U83981	0.003096	0.004342	0.014327	0.28747	PPP1R15A
116_at1755	X14968	0.013622	0.004342	0.004727	0.105215	PRKAR2A
1267_at1756	M55284	0.003096	0.004342	0.003435	-0.17401	PRKCH
35752_s_at1757	M15036	0.003096	0.004342	0.010965	-0.25119	PROS1
40519_at758	Y00638	0.003096	0.004342	0.004977	-0.30956	PTPRC
36204_at759	Y00815	0.003096	0.004342	0.015344	0.116938	PTPRF
1587_at1760	M38258	0.003096	0.004342	0.009252	-0.14193	RARG
35202_at761	AF025654	0.003096	0.004342	0.002302	-0.39122	RNGTT
37946_at762	M60724	0.013622	0.004342	0.004732	-0.22065	RPS6KB1
40467_at763	AB006202	0.013622	0.004342	0.003028	-0.18268	SDHD
4159	AA890010	0.003096	0.004342	0.00546	-0.21285	SEC22L1

8_at~~1~~ ~~764~~						
41352_at~~1~~ ~~765~~	X62822	0.003096	0.004342	0.039707	-0.21593	SIAT1
33649_at~~1~~ ~~766~~	L41680	0.003096	0.004342	0.001771	-0.16486	SIAT8D
1866_g_at ~~1767~~	X15217	0.003096	0.004342	0.007377	0.149306	SKIL
33260_at~~1~~ ~~768~~	L13857	0.003096	0.004342	0.005721	-0.11073	SOS1
1031_at~~17~~ ~~69~~	U09564	0.003096	0.004342	0.001203	-0.27717	SRPK1
39246_at~~1~~ ~~770~~	Z75330	0.013622	0.004342	0.031796	-0.11359	STAG1
37278_at~~1~~ ~~771~~	X92762	0.003096	0.004342	0.001021	-0.27946	TAZ
31742_at~~1~~ ~~772~~	AF064090	0.003096	0.004342	0.006206	0.303013	TNFSF14
471_f_at~~1~~ ~~773~~	U47634	0.003096	0.004342	0.0057	0.278205	TUBB4
33490_at~~1~~ ~~774~~	L27071	0.003096	0.004342	0.000732	-0.39906	TXK
1423_at~~17~~ ~~75~~	D78514	0.003096	0.004342	0.000681	-0.2599	UBE2G1
36378_at~~1~~ ~~776~~	AF085807	0.003096	0.004342	0.005801	0.124457	UPK1A
32086_at~~1~~ ~~777~~	U66561	0.003096	0.004342	0.002542	0.448044	ZNF184
34544_at~~1~~ ~~778~~	X78925	0.013622	0.004342	0.001898	0.351929	ZNF267
1921_at~~17~~ ~~79~~	HG2510- HT2606	0.013622	0.004342	0.007016	0.179499	
36564_at~~1~~ ~~780~~	W27419	0.003096	0.004342	0.006325	0.341787	
37842_at~~1~~ ~~781~~	AF054589	0.003096	0.004342	0.030568	-0.50762	
39103_s_	H98552	0.003096	0.004342	0.017185	-0.1057	

at1782						
40194_at1783	AI056697	0.003096	0.004342	0.000329	-0.20147	
AFFX-HSAC07/X00351_M_st1784	X00351	0.003096	0.005207	0.001506	-0.12928	ACTB
35733_at1785	AF006082	0.003096	0.005207	0.002797	-0.34587	ACTR2
39225_at1786	Y09443	0.003096	0.005207	0.002286	-0.17646	AGPS
33991_g_at1787	U22961	0.003096	0.005207	0.003092	0.147932	ALB
36172_s_at1788	AF002163	0.003096	0.005207	0.002447	-0.37588	AP3D1
36211_at1789	D87461	0.003096	0.005207	0.004809	-0.26338	BCL2L2
37345_at1790	AF013759	0.003096	0.005207	0.004946	-0.18574	CALU
1273_r_at1791	L22005	0.003096	0.005207	0.006442	0.131869	CDC34
34673_r_at1792	AL109689	0.003096	0.005207	0.013291	-0.24945	CGI-142
34707_at1793	U91543	0.003096	0.005207	0.014143	-0.25258	CHD3
38466_at1794	X82153	0.003096	0.005207	0.013882	-0.31742	CTSK
36777_at1795	AJ001687	0.003096	0.005207	0.000224	-0.64837	D12S2489E
31835_at1796	M13149	0.003096	0.005207	0.008717	-0.13824	HRG
37679_at1797	Y10313	0.003096	0.005207	0.006846	0.464769	IFRD1

33281_at798	D63485	0.003096	0.005207	0.000985	-0.31599	IKKE
38892_at799	D87077	0.003096	0.005207	0.043072	-0.21138	KIAA0240
37146_at800	AB007864	0.003096	0.005207	0.001569	0.256672	KIAA0404
1439_s_at1801	X75346	0.003096	0.005207	0.001841	0.331699	MAPKAPK2
654_at1802	L07648	0.003096	0.005207	0.010594	0.226817	MXI1
40344_at803	AB028993	0.003096	0.005207	0.0247	0.133216	NLGN1
39435_at804	D45333	0.003096	0.005207	0.002104	0.302454	PFDN1
1094_g_at1805	M65254	0.003096	0.005207	0.002619	0.262897	PPP2R1B
33265_at806	M86852	0.003096	0.005207	0.004274	0.172251	PXMP3
967_g_at807	X97795	0.003096	0.005207	0.021131	-0.18349	RAD54L
32437_at808	U14970	0.003096	0.005207	0.001894	-0.1353	RPS5
36916_at809	X74570	0.003096	0.005207	0.00345	0.210049	SIAT4C
39537_at810	X98248	0.003096	0.005207	0.010403	-0.50617	SORT1
1640_at1811	U17714	0.003096	0.005207	0.002081	-0.19372	ST13
33989_f_at1812	W28869	0.003096	0.005207	0.001369	-0.38498	TEGT
32314_g_at1813	M12125	0.003096	0.005207	0.000178	-0.09929	TPM2
1600_at1814	L27071	0.003096	0.005207	0.003834	-0.36074	TXK
1947_g_at	M60614	0.003096	0.005207	0.001757	-0.25283	WIT-1

1815						
1515_at1816	HG4074-HT4344	0.003096	0.005207	0.004175	0.589048	
36894_at1817	AL031846	0.003096	0.005207	0.004012	-0.42132	
956_at1818	HG1980-HT2023	0.003096	0.005207	0.002314	0.711234	
34384_at1819	AF022853	0.047678	0.006683	0.002056	-0.30792	ABCC1
41654_at1820	X02994	0.047678	0.006683	0.036598	-0.12393	ADA
37543_at1821	D25304	0.047678	0.006683	0.002258	-0.44746	ARHGEF6
39790_at1822	M23115	0.047678	0.006683	0.016518	-0.1243	ATP2A2
37549_g_at1823	U87408	0.047678	0.006683	0.008628	-0.33961	B1
32606_at1824	AA135683	0.047678	0.006683	0.010045	0.6329	BASP1
31314_at1825	M22491	0.047678	0.006683	0.020141	-0.10386	BMP3
1096_g_at1826	M28170	0.047678	0.006683	0.014303	0.280093	CD19
40738_at1827	M16336	0.047678	0.006683	0.011755	-0.19993	CD2
1942_s_at1828	U37022	0.047678	0.006683	0.028135	-0.06885	CDK4
450_g_at1829	U66469	0.047678	0.006683	0.004123	0.616896	CGR19
39840_at1830	AI037867	0.047678	0.006683	0.009634	-0.11973	CKTSF1B1
31493_s_at1831	J03071	0.047678	0.006683	0.011153	-0.23776	CSH2
594_s_at1832	M55265	0.047678	0.006683	0.01278	-0.1479	CSNK2A1
1492	M33317	0.047678	0.006683	0.014832	-0.17753	CYP2A7

f_at 1833						
500_at1834	U37143	0.013622	0.006683	0.001908	0.171138	CYP2J2
37860_at1835	AL049942	0.013622	0.006683	0.00076	-0.20245	DKFZP564F1422
41018_at1836	AL050015	0.013622	0.006683	0.008524	-0.13959	DKFZP564O243
41124_r_at1837	L35594	0.013622	0.006683	0.002806	0.216985	ENPP2
32343_at1838	J03796	0.047678	0.006683	0.002596	-0.28198	EPB41
35994_at1839	AC002398	0.013622	0.006683	0.003226	-0.27062	F25965
36762_at1840	X15376	0.013622	0.006683	0.014388	-0.15607	GABRG2
31850_at1841	M90656	0.047678	0.006683	0.006961	-0.15968	GCLC
41074_at1842	AF062006	0.013622	0.006683	0.001442	0.200117	GPR49
416_s_at1843	X61755	0.013622	0.006683	0.000491	-0.19331	HOXC5
34764_at1844	D21851	0.047678	0.006683	0.017915	0.153927	KIAA0028
36360_at1845	AB007976	0.047678	0.006683	0.032427	0.228873	KIAA0507
41113_at1846	AI871396	0.047678	0.006683	0.001957	-0.48312	KIAA0557
39924_at1847	AB020660	0.047678	0.006683	0.001858	-0.27616	KIAA0853
36735_f_at1848	X93595	0.047678	0.006683	0.026214	0.245064	KIR3DL2
32116_at1849	AB002405	0.047678	0.006683	0.003681	-0.19481	LAK-4P
38611_at1850	X07228	0.047678	0.006683	0.046458	0.113484	LIPC

34459_at851	U50529	0.047678	0.006683	0.001977	0.310499	LOC88523
38639_at852	AF040963	0.047678	0.006683	0.012629	0.148739	MAD4
1325_at1853	U59423	0.047678	0.006683	0.01126	-0.1341	MADH1
40823_s_at1854	U85430	0.013622	0.006683	0.000224	-0.41454	NFATC3
39137_at855	X80878	0.047678	0.006683	0.010021	-0.16096	NFRKB
337_at1856	AF005043	0.013622	0.006683	0.00078	-0.15296	PARG
31979_at857	D49818	0.047678	0.006683	0.021976	-0.10631	PFKFB4
32904_at858	M28393	0.013622	0.006683	0.003241	-0.16419	PRF1
40518_at859	Y00062	0.047678	0.006683	0.011868	-0.2415	PTPRC
40816_at860	L07758	0.047678	0.006683	0.008943	0.201883	PWP1
809_at1861	U57094	0.047678	0.006683	0.014944	-0.31108	RAB27A
228_at1862	M35416	0.013622	0.006683	0.002789	-0.41233	RALB
41572_r_at1863	X75042	0.047678	0.006683	0.003614	0.659166	REL
40457_at864	AF038250	0.047678	0.006683	0.004198	0.395171	SFRS3
37490_at865	L27213	0.013622	0.006683	0.001014	-0.13065	SLC4A3
32179_s_at1866	Y09568	0.047678	0.006683	0.005799	-0.3407	SNAP23
40150_at867	AA205857	0.013622	0.006683	0.00048	0.27495	SNRPD3
1029	U07794	0.047678	0.006683	0.007632	-0.20733	TXK

s_at 1868						
41377_f_at1869	J05428	0.013622	0.006683	0.00573	-0.08342	UGT2B7
41713_at1870	U09848	0.047678	0.006683	0.011538	-0.26846	ZNF36
36642_at1871	J00287	0.047678	0.006683	0.000953	-0.28381	
39383_at1872	AB007882	0.013622	0.009369	0.006034	-0.17275	ADCY6
32261_at1873	AF072810	0.013622	0.009369	0.016137	-0.32509	BAZ1B
40790_at1874	AB004066	0.013622	0.009369	0.00789	0.494455	BHLHB2
36578_at1875	U37547	0.013622	0.009369	0.00478	0.544595	BIRC2
39109_at1876	AB024704	0.013622	0.009369	0.010893	-0.11914	C20orf1
32177_s_at1877	AC004084	0.013622	0.009369	0.005491	-0.17437	CAPRI
31506_s_at1878	L12691	0.013622	0.009369	0.018291	-0.18848	DEFA3
1272_at1879	L19161	0.013622	0.009369	0.001645	-0.27253	EIF2S3
40067_at1880	M82882	0.013622	0.009369	0.003966	0.478256	ELF1
37318_at1881	X81625	0.013622	0.009369	0.003918	0.762544	ETF1
34959_at1882	M15059	0.013622	0.009369	0.035106	0.313247	FCER2
40772_at1883	AA284298	0.013622	0.009369	0.028745	-0.12535	FLJ22269
37245_at1884	U13044	0.013622	0.009369	0.017986	-0.32813	GABPA
36262_at1	Z12173	0.013622	0.009369	0.001297	-0.32703	GNS

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39823_at~~886~~	U06631	0.013622	0.009369	0.003506	-0.37935	H326
38661_at~~887~~	X75315	0.013622	0.009369	0.002959	1.06191	HSRNASEB
41775_at~~888~~	AF064084	0.013622	0.009369	0.017927	-0.10308	ICMT
38030_at~~889~~	AB002330	0.013622	0.009369	0.048512	-0.09076	KIAA0332
41788_i_at~~1890~~	AB014569	0.013622	0.009369	0.010011	0.709572	KIAA0669
34751_at~~891~~	AI970189	0.013622	0.009369	0.001778	0.569801	KIAA0997
40829_at~~892~~	AB028960	0.013622	0.009369	0.001825	-0.15403	KIAA1037
37778_at~~893~~	AJ005273	0.013622	0.009369	0.001449	0.379277	KIN
32855_at~~894~~	L00352	0.013622	0.009369	0.004231	0.554465	LDLR
33447_at~~895~~	X54304	0.013622	0.009369	0.000863	-0.19567	MLCB
40626_at~~896~~	AI693193	0.013622	0.009369	0.023978	-0.25831	MTX1
33002_at~~897~~	AF047487	0.013622	0.009369	0.001312	-0.33746	NCK2
40122_at~~898~~	AF037448	0.013622	0.009369	0.00743	0.204106	NSAP1
41202_s_at~~1899~~	AF000152	0.013622	0.009369	0.025216	-0.34592	OS4
38526_at~~900~~	U02882	0.013622	0.009369	0.017536	0.892321	PDE4D
392_g_at~~901~~	X89416	0.013622	0.009369	0.005129	-0.1405	PPP5C
1043_s_at~~1902~~	U27516	0.013622	0.009369	0.004164	-0.17553	RAD52
3348	D23660	0.013622	0.009369	0.01215	0.149327	RPL4

5_at~~1~~ ~~903~~						
33421_s_at~~1904~~	AB016247	0.013622	0.009369	0.019879	0.416634	SC5DL
35488_at~~1905~~	U44754	0.013622	0.009369	0.005273	0.158396	SNAPC1
41871_at~~1906~~	AI660929	0.013622	0.009369	0.000698	-0.15764	T1A-2
37324_at~~1907~~	X01060	0.013622	0.009369	0.005079	0.27369	TFRC
33803_at~~1908~~	J02973	0.013622	0.009369	0.006825	0.835338	THBD
1729_at~~1909~~	L41690	0.013622	0.009369	0.020209	-0.32814	TRADD
39123_s_at~~1910~~	X89066	0.013622	0.009369	0.000396	-0.2226	TRPC1
34402_at~~1911~~	AB024327	0.013622	0.009369	0.031	0.260875	UNRIP
34001_at~~1912~~	AF033199	0.013622	0.009369	0.02842	-0.1806	ZNF204
39218_at~~1913~~	AL080123	0.013622	0.009369	0.018447	0.215445	ZNF23
39762_at~~1914~~	AB007885	0.013622	0.009369	0.025803	-0.22701	ZNF262
834_at~~1915~~	U40462	0.013622	0.009369	0.004101	-0.29722	ZNFN1A1
1146_at~~1916~~	HG3477-HT3670	0.013622	0.009369	0.00042	-0.2367	
253_g_at~~1917~~	L42324	0.013622	0.009369	0.015195	0.283048	GPR18
31736_at~~1918~~	AA975427	0.013622	0.009369	0.002377	-0.26992	
39170_at~~1919~~	AL049957	0.013622	0.009369	0.007809	0.133451	
40720_at~~1920~~	AL022398	0.013622	0.009369	0.017529	-0.48579	

694_at1921	HG2689-HT2785	0.013622	0.009369	0.029818	0.202486	
41565_at1922	AF034373	0.013622	0.014679	0.00591	-0.26511	A2LP
37038_at1923	X83467	0.013622	0.014679	0.006111	-0.25837	ABCD3
34761_r_at1924	U41766	0.047678	0.014679	0.014363	0.473526	ADAM9
33102_at1925	D67031	0.013622	0.014679	0.007826	-0.4645	ADD3
38253_at1926	U84011	0.013622	0.014679	0.012995	-0.2499	AGL
1912_s_at1927	M74088	0.013622	0.014679	0.038601	-0.16952	APC
1863_s_at1928	U67092	0.047678	0.014679	0.047381	-0.10935	ATM
38663_at1929	AI033692	0.047678	0.014679	0.010056	-0.2417	BCRP1
394_at1930	X92106	0.013622	0.014679	0.001377	-0.33994	BLMH
39565_at1931	Z22535	0.047678	0.014679	0.021613	-0.09832	BMPR1A
38740_at1932	X79067	0.047678	0.014679	0.0381	0.14954	BRF1
33864_at1933	X86098	0.013622	0.014679	0.000807	-0.34829	BS69
36634_at1934	U72649	0.047678	0.014679	0.029157	0.227444	BTG2
39782_at1935	X95592	0.047678	0.014679	0.014127	0.201273	C1D
32031_at1936	D78586	0.047678	0.014679	0.028845	-0.05709	CAD
1421_at1937	D30742	0.047678	0.014679	0.028215	0.180381	CAMK4
31854_at1938	AF035582	0.047678	0.014679	0.002042	0.530946	CASK

487_g_at~~1~~ 939	U60521	0.047678	0.014679	0.002353	0.552837	CASP9
37009_at~~1~~ 940	AL035079	0.013622	0.014679	0.00063	-0.78567	CAT
39562_at~~1~~ 941	AF094481	0.047678	0.014679	0.024569	0.149973	CGGBP1
34200_at~~1~~ 942	X83378	0.013622	0.014679	0.025603	0.133485	CLCN6
36080_at~~1~~ 943	AB002332	0.047678	0.014679	0.003136	-0.20009	CLOCK
39768_at~~1~~ 944	D13146	0.013622	0.014679	0.017967	-0.13385	CNP
35955_at~~1~~ 945	S80864	0.013622	0.014679	0.011106	-0.33164	CYCL
37981_at~~1~~ 946	D17530	0.047678	0.014679	0.005519	-0.15234	DBN1
39182_at~~1~~ 947	U87947	0.047678	0.014679	0.011279	0.222382	EMP3
37986_at~~1~~ 948	M60459	0.047678	0.014679	0.010174	-0.10156	EPOR
32731_at~~1~~ 949	AB018247	0.013622	0.014679	0.000348	0.423577	FE65L2
32187_at~~1~~ 950	AB028973	0.013622	0.014679	0.046458	-0.12088	FLJ10883
41406_at~~1~~ 951	AL080172	0.047678	0.014679	0.02693	-0.063	FLJ21919
34740_at~~1~~ 952	AF032886	0.047678	0.014679	0.009814	0.232307	FOXO3A
39181_at~~1~~ 953	U00928	0.047678	0.014679	0.01307	-0.0915	FUS
909_g_at~~1~~ 954	M14660	0.047678	0.014679	0.011038	0.732462	FUT10
36484_at~~1~~ 955	AI935146	0.047678	0.014679	0.044653	0.246267	GALNT3
37706_at~~1~~ 956	U28811	0.047678	0.014679	0.007572	-0.21558	GLG1
3543	AF001903	0.013622	0.014679	0.001957	-0.28636	HADHSC

5_s_at1957						
102_at1958	Y09306	0.047678	0.014679	0.045083	-0.08024	HIPK3
40369_f_at1959	AL022723	0.047678	0.014679	0.041021	0.165267	HLA-G
35017_f_at1960	M80469	0.013622	0.014679	0.037453	-0.12099	HLA-J
37618_at1961	M16937	0.013622	0.014679	0.002262	-0.13536	HOXB7
31541_at1962	X98307	0.013622	0.014679	0.011852	-0.0908	HSHUR7SEQ
1179_at1963	HG2855-HT2995	0.047678	0.014679	0.030595	0.16813	HSP70
36614_at1964	X87949	0.047678	0.014679	0.028569	0.296273	HSPA5
32736_at1965	W68830	0.013622	0.014679	0.007971	-0.22855	HSPC022
1185_at1966	D49410	0.047678	0.014679	0.040369	0.153358	HUMIL3RA12
35815_at1967	AL049470	0.013622	0.014679	0.010492	0.283688	HYPB
35797_at1968	Y10659	0.047678	0.014679	0.024205	-0.1217	IL13RA1
37603_at1969	X52015	0.047678	0.014679	0.006637	0.417081	IL1RN
35539_at1970	AF047492	0.047678	0.014679	0.002557	0.25738	IMPG1
33507_g_at1971	U96919	0.013622	0.014679	0.003221	-0.19947	INPP4A
36074_at1972	U12897	0.013622	0.014679	0.002496	-0.15016	IPW
41049_at1973	S62539	0.013622	0.014679	0.012982	-0.20615	IRS1
3213	AF029778	0.047678	0.014679	0.018006	-0.14486	JAG2

7_at~~1~~ 974						
33363_at~~1~~ 975	W25934	0.047678	0.014679	0.016925	0.363279	JTV1
1612_s_at ~~1976~~	X56681	0.047678	0.014679	0.004935	0.713663	JUND
38197_at~~1~~ 977	M64934	0.047678	0.014679	0.003162	-0.1823	KEL
34844_at~~1~~ 978	D86975	0.047678	0.014679	0.048475	0.163408	KIAA0222
31982_at~~1~~ 979	AB020701	0.013622	0.014679	0.013946	0.283086	KIAA0894
35878_at~~1~~ 980	AB023141	0.047678	0.014679	0.017326	-0.33543	KIAA0924
32735_at~~1~~ 981	AB023148	0.013622	0.014679	0.016218	-0.27496	KIAA0931
34712_at~~1~~ 982	AB023227	0.047678	0.014679	0.043542	0.316063	KIAA1010
32693_at~~1~~ 983	AB028963	0.047678	0.014679	0.039194	-0.12296	KIAA1040
37857_at~~1~~ 984	AL080188	0.047678	0.014679	0.016745	-0.10387	KIAA1775
36717_at~~1~~ 985	AJ224162	0.013622	0.014679	0.002225	-0.24337	LAS
288_s_at~~1~~ 986	L25931	0.013622	0.014679	0.00482	-0.2367	LBR
35426_at~~1~~ 987	AC004410	0.047678	0.014679	0.017457	0.210096	LOC56928
31815_r_at~~1988~~	AB009462	0.047678	0.014679	0.012892	0.131673	LRP3
41831_at~~1~~ 989	AF077820	0.013622	0.014679	0.003095	-0.40005	LRP5
38441_s_at~~1990~~	X59408	0.047678	0.014679	0.018321	-0.3029	MCP
39037_at~~1~~ 991	L13773	0.013622	0.014679	0.002741	-0.18297	MLLT2

37283_at~~1992~~	X82209	0.047678	0.014679	0.010828	0.178564	MN1
35145_at~~1993~~	X96401	0.013622	0.014679	0.001643	0.317165	MNT
879_at~~1994~~	M30818	0.047678	0.014679	0.032832	0.292682	MX2
37724_at~~1995~~	V00568	0.013622	0.014679	0.008535	-0.58978	MYC
1904_at~~1996~~	D50692	0.013622	0.014679	0.043374	-0.20783	MYCBP
37250_at~~1997~~	AB007191	0.013622	0.014679	0.022026	-0.18098	MYCBP
989_at~~1998~~	X17576	0.013622	0.014679	0.001641	-0.26027	NCK1
40362_at~~1999~~	X61498	0.013622	0.014679	0.006234	0.307667	NFKB2
39161_at~~2000~~	AF052093	0.047678	0.014679	0.001318	-0.31976	NJMU-R1
430_at~~2001~~	X00737	0.047678	0.014679	0.037385	0.219194	NP
33849_at~~2002~~	U02020	0.047678	0.014679	0.014866	0.650286	PBEF
1223_at~~2003~~	X66362	0.047678	0.014679	0.006159	0.137944	PCTK3
38365_at~~2004~~	AF026086	0.047678	0.014679	0.006555	-0.18222	PEX1
1275_at~~2005~~	L25441	0.047678	0.014679	0.011907	0.146471	PGGT1B
40446_at~~2006~~	AL021366	0.013622	0.014679	0.002775	0.425217	PHF1
751_at~~2007~~	D85418	0.013622	0.014679	0.004449	-0.31688	PIGC
353_at~~2008~~	D30037	0.047678	0.014679	0.001579	-0.21226	PITPNB
32775_r_at~~2009~~	AB006746	0.047678	0.014679	0.0356	0.189986	PLSCR1

32167_at2010	AF054182	0.013622	0.014679	0.002098	-0.54761	PMPCB
857_at2011	S87759	0.013622	0.014679	0.007522	0.39052	PPM1A
31635_g_at2012	M13057	0.047678	0.014679	0.032523	-0.19317	PRH1
38371_at2013	M64992	0.047678	0.014679	0.047326	0.178696	PSMA1
31892_at2014	X58288	0.047678	0.014679	0.002633	0.409542	PTPRM
1753_s_at2015	AD000092	0.047678	0.014679	0.028359	0.137917	RAD23A
37530_s_at2016	U79716	0.013622	0.014679	0.003409	0.195389	RELN
41705_at2017	U69198	0.047678	0.014679	0.048001	0.085316	RFNG
41384_at2018	AF117829	0.047678	0.014679	0.003668	0.377251	RIPK2
33342_at2019	AF039029	0.047678	0.014679	0.002146	-0.28622	RNUT1
41277_at2020	AW021542	0.013622	0.014679	0.000677	-0.29232	SAP18
40385_at2021	U64197	0.047678	0.014679	0.021124	0.220476	SCYA20
36316_r_at2022	AB023136	0.013622	0.014679	0.00288	-0.10963	SEC15B
37597_s_at2023	AF055006	0.013622	0.014679	0.011241	0.238955	SEC6
34327_at2024	Z46606	0.047678	0.014679	0.005778	-0.1566	SMARCA3
33268_at2025	L25270	0.047678	0.014679	0.002401	-0.15644	SMCX
37353_g_at2026	M60618	0.013622	0.014679	0.006316	0.235838	SP100

32038_s_at2027	AI739308	0.013622	0.014679	0.001861	-0.57419	SRP46
34356_at2028	U52960	0.047678	0.014679	0.02599	0.429086	SURB7
37553_at2029	D50863	0.013622	0.014679	0.006582	-0.13005	TESK1
41762_at2030	D64015	0.013622	0.014679	0.007587	-0.3629	TIAL1
38303_at2031	AB001523	0.047678	0.014679	0.027565	0.164838	TMEM1
38457_at2032	L21715	0.013622	0.014679	0.000862	0.309808	TNNI2
31943_g_at2033	AF045583	0.047678	0.014679	0.043887	-0.16757	TULP3
31882_at2034	AJ001340	0.013622	0.014679	0.002396	-0.17031	U3-55K
34824_at2035	AB015344	0.013622	0.014679	0.008107	-0.31161	UBQLN2
36653_g_at2036	J03824	0.013622	0.014679	0.005864	-0.18849	UROS
34803_at2037	AF022789	0.047678	0.014679	0.006582	0.309267	USP12
1926_at2038	U48801	0.013622	0.014679	0.003849	-0.17743	VEGFB
1665_s_at2039	HG544-HT544	0.047678	0.014679	0.010549	0.454218	
31618_at2040	S66666	0.013622	0.014679	0.003364	-0.14303	
32815_at2041	AI687419	0.047678	0.014679	0.039394	-0.3657	
33648_at2042	W28800	0.047678	0.014679	0.004582	0.270831	
34752_at2043	AL080111	0.013622	0.014679	0.001378	-0.36029	
3493	AF070536	0.047678	0.014679	0.006685	0.199364	

9_r_at2044						
36071_at2045	AF070633	0.047678	0.014679	0.010142	-0.1635	
36368_at2046	AF054998	0.013622	0.014679	0.007913	-0.21157	
701_s_at2047	HG3725-HT3981	0.047678	0.014679	0.027792	-0.11953	
954_s_at2048	HG1614-HT1614	0.013622	0.014679	0.006999	-0.45233	
39385_at2049	M22324	0.013622	0.01669	0.009982	0.283293	ANPEP
32490_at2050	AC005955	0.013622	0.01669	0.004346	0.137324	CEACAM4
32066_g_at2051	S68134	0.013622	0.01669	0.005372	1.92718	CREM
32067_at2052	S68271	0.013622	0.01669	0.009154	1.49785	CREM
39839_at2053	M24069	0.013622	0.01669	0.003022	0.249971	CSDA
38355_at2054	AF000984	0.013622	0.01669	0.004295	0.46432	DBY
35571_at2055	AF055917	0.013622	0.01669	0.015434	0.102855	F2RL3
36289_f_at2056	U27333	0.013622	0.01669	0.012662	0.136047	FUT6
32706_at2057	X89887	0.013622	0.01669	0.009728	0.152829	HIRA
1568_s_at2058	L42243	0.013622	0.01669	0.002638	0.218644	IFNAR2
35850_at2059	AI950382	0.013622	0.01669	0.00744	0.601631	KIAA0585
35851_g_at2060	AI950382	0.013622	0.01669	0.002126	0.519735	KIAA0585
3692	U17760	0.013622	0.01669	0.044392	0.431131	LAMB3

9_at2061						
33720_at2062	L48692	0.013622	0.01669	0.041233	0.63409	LOC56902
37406_at2063	X94232	0.013622	0.01669	0.016402	0.326694	MAPRE2
41063_g_at2064	AA037278	0.013622	0.01669	0.01607	0.119411	MGC10882
280_g_at2065	L13740	0.013622	0.01669	0.007795	0.355688	NR4A1
40659_at2066	U12767	0.013622	0.01669	0.011648	1.30268	NR4A3
40661_at2067	D78579	0.013622	0.01669	0.005896	1.11766	NR4A3
32227_at2068	X17042	0.013622	0.01669	0.015594	0.239796	PRG1
843_at2069	U48296	0.013622	0.01669	0.003124	0.864101	PTP4A1
570_at2070	M83221	0.013622	0.01669	0.012321	0.192956	RELB
38040_at2071	AF107463	0.013622	0.01669	0.009662	0.419254	SPF30
904_s_at2072	L47276	0.013622	0.01669	0.004673	0.194449	TOP2A
429_f_at2073	X00734	0.013622	0.01669	0.010039	0.347307	TUBB5
40103_at2074	X51521	0.013622	0.01669	0.010303	0.60161	VIL2
33658_at2075	S54641	0.013622	0.01669	0.008483	0.183207	ZNF124
38417_at2076	M91029	0.013622	0.022759	0.010686	0.450612	AMPD2
38550_at2077	AB021638	0.136189	0.022759	0.024881	-0.1126	APBA3
36872_at2078	AL120559	0.013622	0.022759	0.004505	0.577915	ARPP-19
3260	AF039656	0.013622	0.022759	0.006991	0.68481	BASP1

7_at2079						
34286_at2080	AB020623	0.047678	0.022759	0.009696	0.418826	BCAS2
40023_at2081	X60201	0.013622	0.022759	0.011758	-0.1576	BDNF
40910_at2082	U56637	0.047678	0.022759	0.008899	-0.28102	CAPZA1
37572_at2083	AW043690	0.047678	0.022759	0.031971	0.134862	CCK
39767_at2084	D13627	0.047678	0.022759	0.019298	0.203913	CCT8
806_at2085	U56998	0.013622	0.022759	0.024403	0.442545	CNK
32820_at2086	U71267	0.047678	0.022759	0.007233	-0.13426	CNOT4
38660_at2087	F27891	0.047678	0.022759	0.02847	0.119514	COX6A2
36573_at2088	U78524	0.013622	0.022759	0.002554	0.353034	DDXBP1
40494_at2089	AF043733	0.047678	0.022759	0.005645	0.22771	DEDD
38992_at2090	X64229	0.013622	0.022759	0.013033	-0.20244	DEK
34151_at2091	AL050284	0.047678	0.022759	0.002819	0.232244	DKFZP586M1019
41226_at2092	L05147	0.013622	0.022759	0.021168	0.111752	DUSP3
1639_s_at2093	U15642	0.013622	0.022759	0.013339	0.474421	E2F5
41275_at2094	U31556	0.047678	0.022759	0.011303	0.335871	E2F5
31965_at2095	AC004262	0.047678	0.022759	0.004968	-0.25642	EMR2
35972_at2096	AA181196	0.047678	0.022759	0.009459	-0.10534	FLJ11712
34715_at2	U74612	0.013622	0.022759	0.014802	-0.18783	FOXM1

097						
35785_at2098	W28281	0.013622	0.022759	0.011042	0.813742	GABARAPL1
35942_at2099	AI183417	0.013622	0.022759	0.011016	0.117979	GABPB1
1598_g_at2100	L13720	0.013622	0.022759	0.014471	-0.1601	GAS6
35130_at2101	X15722	0.013622	0.022759	0.029451	-0.19175	GSR
41371_at2102	Y07595	0.013622	0.022759	0.003113	-0.20996	GTF2H4
37574_at2103	L43821	0.047678	0.022759	0.005863	-0.20401	HEF1
33123_at2104	L10379	0.013622	0.022759	0.02006	-0.15961	HRIHFB2206
39348_at2105	X99209	0.013622	0.022759	0.021333	-0.14942	HRMT1L1
36617_at2106	X77956	0.013622	0.022759	0.009598	0.591031	ID1
34333_at2107	AL021707	0.013622	0.022759	0.004161	1.79061	KIAA0063
38984_at2108	AB007896	0.013622	0.022759	0.006273	-0.41247	KIAA0436
39953_i_at2109	AB014528	0.047678	0.022759	0.001992	-0.31837	KIAA0628
32405_at2110	AB014607	0.013622	0.022759	0.000764	-0.15753	KIAA0707
38424_at2111	AB018290	0.013622	0.022759	0.034506	-0.28703	KIAA0747
41691_at2112	AB018337	0.013622	0.022759	0.008466	-0.41118	KIAA0794
37081_at2113	AB023161	0.013622	0.022759	0.018461	-0.15095	KIAA0944
41001_at2114	AB023202	0.013622	0.022759	0.005879	-0.19156	KIAA0985
34815_at2	U80743	0.013622	0.022759	0.000544	-0.30322	KIAA1498

~~115~~						
33820_g_at~~2116~~	X13794	0.047678	0.022759	0.018671	-0.12764	LDHB
38390_at~~2117~~	Z34975	0.013622	0.022759	0.012256	-0.29089	LDLC
40059_r_at~~2118~~	AI341656	0.047678	0.022759	0.021482	-0.26002	LIM
35630_at~~2119~~	X87342	0.013622	0.022759	0.006652	-0.23382	LLGL2
2004_at~~2120~~	U29671	0.047678	0.022759	0.001133	-0.2617	MAP3K1
34770_at~~2121~~	Z14138	0.013622	0.022759	0.00408	0.81232	MAP3K8
35339_at~~2122~~	AI743606	0.013622	0.022759	0.00269	-0.19764	MEL
38987_at~~2123~~	AF052183	0.013622	0.022759	0.002151	-0.19631	MGC2722
38325_at~~2124~~	AL050356	0.013622	0.022759	0.002743	-0.42417	MINPP1
40878_f_at~~2125~~	AF041081	0.013622	0.022759	0.019282	-0.21627	MN7
484_at~~2126~~	U59302	0.013622	0.022759	0.003859	0.280175	NCOA1
39040_at~~2127~~	W28360	0.013622	0.022759	0.016633	0.272057	NCUBE1
32639_at~~2128~~	U97198	0.013622	0.022759	0.001352	-0.20163	NLP_1
41282_s_at~~2129~~	AA194159	0.013622	0.022759	0.004614	-0.40044	PEX10
178_f_at~~2130~~	U38964	0.013622	0.022759	0.004912	-0.23793	PMS2L8
1875_f_at~~2131~~	D38498	0.013622	0.022759	0.003965	-0.58306	PMS2L9
35858_at~~2~~	AA996066	0.013622	0.022759	0.003514	-0.21994	PMS2L9

~~132~~						
33457_at~~133~~	AB029028	0.013622	0.022759	0.027753	-0.29778	RAP140
40261_at~~134~~	AA402524	0.047678	0.022759	0.005359	-0.11564	RBM9
39841_at~~135~~	U79745	0.013622	0.022759	0.00409	0.777629	SLC16A6
35113_at~~136~~	X98332	0.013622	0.022759	0.002282	-0.20078	SLC22A1
32074_at~~137~~	D42045	0.013622	0.022759	0.006867	-0.19726	SNM1
32108_at~~138~~	M76231	0.013622	0.022759	0.009942	0.13899	SPR
40596_at~~139~~	U76366	0.013622	0.022759	0.015416	-0.09378	TCOF1
32682_at~~140~~	U09087	0.013622	0.022759	0.00607	-0.26017	TMPO
37750_at~~141~~	AF049140	0.047678	0.022759	0.011115	-0.21894	UBE2V2
36102_at~~142~~	AF038962	0.047678	0.022759	0.007219	-0.44337	VDAC3
34781_at~~143~~	D84145	0.013622	0.022759	0.002923	0.574155	WS-3
41532_at~~144~~	Y09723	0.047678	0.022759	0.001292	0.234149	ZNF151
32926_at~~145~~	AL049991	0.013622	0.022759	0.007094	0.245237	
35645_at~~146~~	AL050148	0.013622	0.022759	0.013128	-0.26398	
38623_at~~147~~	AI014538	0.013622	0.022759	0.003507	-0.15278	
40177_at~~148~~	AI732885	0.047678	0.022759	0.043886	-0.10293	
AFFX-hum_alu_at~~2149~~	U14573	0.013622	0.022759	0.04259	-0.11614	

1700_at~~2150~~	U82987	0.013622	0.024606	0.00343	-0.17272	BBC3
935_at~~2151~~	L12168	0.013622	0.024606	0.007944	-0.22028	CAP
40382_at~~152~~	V00571	0.013622	0.024606	0.005873	0.132015	CRH
40719_at~~153~~	AL022398	0.013622	0.024606	0.015005	-0.44535	DJ434O14.3
35799_at~~154~~	AL080081	0.013622	0.024606	0.007659	0.548836	DNAJB9
40419_at~~155~~	X85116	0.013622	0.024606	0.039531	-0.24601	EPB72
37584_at~~156~~	AJ007669	0.013622	0.024606	0.019404	-0.23162	FANCG
41177_at~~157~~	AW024285	0.013622	0.024606	0.007049	0.311562	FLJ12443
34662_at~~158~~	W27666	0.013622	0.024606	0.009544	-0.25685	FLJ14393
41274_at~~159~~	AA908993	0.013622	0.024606	0.015356	-0.12684	FLJ14393
41323_at~~160~~	U90917	0.013622	0.024606	0.016602	-0.23386	FOXM1
38139_at~~161~~	AF017445	0.013622	0.024606	0.025525	-0.33517	FPGT
36515_at~~162~~	AJ238764	0.013622	0.024606	0.030667	0.197763	GNE
37299_at~~163~~	J04501	0.013622	0.024606	0.007821	-0.23523	GYS1
32321_at~~164~~	X56841	0.013622	0.024606	0.022605	-0.23469	HLA-E
38194_s_at~~2165~~	M63438	0.013622	0.024606	0.005389	-0.75873	IGKC
33410_at~~166~~	S66213	0.013622	0.024606	0.011362	-0.09802	ITGA6
40018_at~~167~~	AB007870	0.013622	0.024606	0.002855	0.657213	KIAA0410

41258_at168	N29665	0.013622	0.024606	0.008301	-0.49779	KIAA0618
36588_at169	AB018353	0.013622	0.024606	0.033864	-0.3542	KIAA0810
32434_at170	D10522	0.013622	0.024606	0.028464	0.22227	MACS
33245_at171	AF004709	0.013622	0.024606	0.018118	-0.09931	MAPK13
41843_r_at2172	W28275	0.013622	0.024606	0.005871	-0.27591	MGC11061
33769_at173	AF087020	0.013622	0.024606	0.032064	-0.13544	MPZL1
1719_at2174	U61981	0.013622	0.024606	0.012069	-0.20932	MSH3
40571_at175	U90942	0.013622	0.024606	0.004002	0.179029	MYO5A
743_at2176	D50370	0.013622	0.024606	0.008327	-0.11492	NAP1L3
41475_at177	U91512	0.013622	0.024606	0.00493	0.549889	NINJ1
39735_at178	AF069987	0.013622	0.024606	0.007336	-0.16953	NIT1
1248_at2179	U37689	0.013622	0.024606	0.007097	-0.17369	POLR2H
1295_at2180	L19067	0.013622	0.024606	0.006406	0.148517	RELA
37585_at181	X13482	0.013622	0.024606	0.016873	0.241998	SNRPA1
778_s_at182	D16827	0.013622	0.024606	0.004314	-0.16954	SSTR5
38822_at183	AB011420	0.013622	0.024606	0.030791	0.171669	STK17A
35006_at184	L39060	0.013622	0.024606	0.026797	-0.24028	TAF1A
32802_at185	AB011169	0.013622	0.024606	0.004017	-0.24355	TEB4

1328_at2186	U69108	0.013622	0.024606	0.024472	-0.17595	TRAF5
41242_at2187	AB011004	0.013622	0.024606	0.00265	1.03158	UAP1
33884_s_at2188	AB014584	0.013622	0.024606	0.028525	-0.1337	UBE4B
1790_s_at2189	HG3914-HT4184	0.013622	0.024606	0.025854	-0.12454	
33588_at2190	Z32860	0.013622	0.024606	0.002037	-0.11041	
36611_at2191	U25849	0.013622	0.024606	0.00632	-0.43498	
36818_at2192	AF052100	0.013622	0.024606	0.006718	-0.2297	
37381_g_at2193	X59268	0.013622	0.024606	0.003586	0.479423	GTF2B
38764_at2194	AF007142	0.013622	0.024606	0.01864	-0.34584	
40642_at2195	AI312646	0.013622	0.024606	0.027596	-0.14991	
37939_at2196	AL022318	0.047678	0.028192	0.049355	-0.11704	APOBEC1L
34898_at2197	M30704	0.047678	0.028192	0.00926	0.279668	AREG
35968_s_at2198	AF001307	0.047678	0.028192	0.018109	-0.12594	ARNT
36463_at2199	AB020680	0.047678	0.028192	0.007009	0.227256	BAG5
37274_at2200	AF018631	0.047678	0.028192	0.008344	-0.13689	BTD
37218_at2201	D64110	0.047678	0.028192	0.022809	0.398412	BTG3
37536_at2202	Z11697	0.047678	0.028192	0.024131	0.750492	CD83
3969	M31516	0.047678	0.028192	0.021562	0.517068	DAF

5_at2203						
39744_at2204	AF000982	0.047678	0.028192	0.025357	0.29808	DDX3
32032_at2205	L77566	0.047678	0.028192	0.01243	0.178957	DGSI
40154_at2206	AL096725	0.047678	0.028192	0.007381	0.436688	DKFZP434B103
37564_at2207	AL080201	0.047678	0.028192	0.044829	-0.11576	DKFZP434F162
36961_at2208	AL050286	0.047678	0.028192	0.004267	-0.22397	DKFZP586A011
34201_at2209	Y13350	0.047678	0.028192	0.015562	0.137002	DNAJA2
41067_at2210	AJ223333	0.047678	0.028192	0.013836	-0.17437	DNMT2
267_at2211	L34075	0.047678	0.028192	0.013848	-0.25236	FRAP1
34332_at2212	D31766	0.047678	0.028192	0.029287	-0.09623	GNPI
31693_f_at2213	Z80776	0.047678	0.028192	0.002034	0.143491	H2AFG
1122_f_at2214	K03183	0.047678	0.028192	0.040298	0.163306	HUMCGBBA3
1501_at2215	X57025	0.047678	0.028192	0.009135	0.437394	IGF1
41483_s_at2216	X56681	0.047678	0.028192	0.012885	0.423181	JUND
41243_at2217	AB007916	0.047678	0.028192	0.00772	-0.45744	KIAA0447
33407_at2218	AI672098	0.047678	0.028192	0.014331	0.160649	KIAA0934
33219_at2219	AB029020	0.047678	0.028192	0.035285	-0.3101	KIAA1097
39163_at2220	W27233	0.047678	0.028192	0.019918	-0.24802	KIDINS220

35139_at221	AL049341	0.047678	0.028192	0.001943	-0.3086	LOC57209
37297_at222	AL049422	0.047678	0.028192	0.028823	0.264129	LOC84549
1857_at223	AF010193	0.047678	0.028192	0.003729	0.927225	MADH7
41279_f_at2224	AF007134	0.047678	0.028192	0.009151	-0.1209	MAPK8IP1
1124_at225	L04731	0.047678	0.028192	0.025599	-0.07236	MLL
39707_at226	AB014547	0.047678	0.028192	0.023787	-0.15831	MTMR4
38276_at227	U91616	0.047678	0.028192	0.018681	0.377931	NFKBIE
37623_at228	X75918	0.047678	0.028192	0.019713	1.21948	NR4A2
37518_at229	AL049842	0.047678	0.028192	0.022698	0.201258	NUFIP1
33628_g_at2230	U57843	0.047678	0.028192	0.011796	-0.13969	PIK3CD
546_at2231	S76965	0.047678	0.028192	0.012413	0.426208	PKIA
37189_at232	AL023553	0.047678	0.028192	0.00321	-0.15608	PMM1
1463_at233	M93425	0.047678	0.028192	0.019899	-0.36854	PTPN12
32156_at234	AF044968	0.047678	0.028192	0.006887	0.121898	PVRL2
621_at2235	M28211	0.047678	0.028192	0.050065	-0.08518	RAB4
38762_at236	AF083255	0.047678	0.028192	0.021248	-0.27368	RNAHP
32899_s_at2237	U04897	0.047678	0.028192	0.013893	0.278167	RORA
3265	AL031228	0.047678	0.028192	0.020491	-0.22382	SACM2L

8_at238						
36998_s_at2239	Y08262	0.047678	0.028192	0.008184	-0.34195	SCA2
38110_at240	AF000652	0.047678	0.028192	0.001533	0.415218	SDCBP
34189_at241	D31891	0.047678	0.028192	0.00536	-0.18144	SETDB1
35883_at242	X66079	0.047678	0.028192	0.008707	0.129642	SPIB
32201_at243	Z96932	0.047678	0.028192	0.013622	-0.14003	SSNA1
33873_at244	D43642	0.047678	0.028192	0.015302	-0.26409	TCFL1
33253_at245	D50919	0.047678	0.028192	0.016207	-0.23972	TRIM14
40567_at246	X01703	0.047678	0.028192	0.004339	0.386096	TUBA3
36100_at247	AF022375	0.047678	0.028192	0.015198	0.503607	VEGF
41542_at248	AF062346	0.047678	0.028192	0.014763	0.455053	ZNF216
31697_s_at2249	J04755	0.047678	0.028192	0.014444	0.302274	
32878_f_at2250	AA524802	0.047678	0.028192	0.036226	-0.24775	
39223_at251	AL096749	0.047678	0.028192	0.017041	0.106309	
38680_at252	M21259	0.047678	0.028192	0.025927	0.18378	
36902_at253	X61587	0.047678	0.037364	0.024028	0.222788	ARHG
37661_at254	J04027	0.047678	0.037364	0.019918	0.336927	ATP2B1
33174_s_	W28091	0.047678	0.037364	0.016936	-0.1567	BBS4

at2255						
2031_s_at2256	U03106	0.047678	0.037364	0.004064	0.915096	CDKN1A
40149_at2257	AL049924	0.047678	0.037364	0.001517	-0.23208	DKFZP547G1110
35934_at2258	L19161	0.047678	0.037364	0.006578	-0.49859	EIF2S3
39390_at2259	AF052123	0.136189	0.037364	0.013524	-0.24445	FLJ10814
39827_at2260	AA522530	0.047678	0.037364	0.038021	0.413536	FLJ20500
35769_at2261	AJ011001	0.047678	0.037364	0.016436	-0.63045	GPR56
476_s_at2262	U50079	0.047678	0.037364	0.013178	-0.37546	HDAC1
40219_at2263	AI796944	0.047678	0.037364	0.011597	0.216392	HIS1
40674_s_at2264	S82986	0.047678	0.037364	0.006441	-0.20652	HOXC6
41122_at2265	AB011173	0.047678	0.037364	0.01376	-0.26283	KIAA0601
37041_at2266	AB023160	0.047678	0.037364	0.029467	-0.23276	KIAA0943
32288_r_at2267	AJ001685	0.047678	0.037364	0.015208	-0.48906	KLRC3
33531_at2268	AJ000673	0.047678	0.037364	0.009021	-0.38103	KLRD1
38500_at2269	AB002450	0.047678	0.037364	0.003391	-0.37426	LOC51014
37486_f_at2270	U68385	0.047678	0.037364	0.007651	-0.16327	MEIS3
40547_at2271	AI688516	0.047678	0.037364	0.017859	-0.15146	NDUFA2
32651_at2	W28770	0.047678	0.037364	0.005269	-0.16121	NP25

272						
32719_at273	L41827	0.047678	0.037364	0.011308	0.139896	NRG1
40088_at274	X84373	0.047678	0.037364	0.00725	0.77533	NRIP1
1115_at2275	M25897	0.047678	0.037364	0.025747	-0.41462	PF4
475_at2276	U50062	0.047678	0.037364	0.018154	0.19401	RIPK1
32364_at277	AJ011785	0.047678	0.037364	0.017907	-0.07616	SIX6
33131_at278	X70683	0.047678	0.037364	0.0155	-0.10219	SOX4
31797_at279	AL035699	0.047678	0.037364	0.006561	-0.15185	TBPL1
33439_at280	D15050	0.047678	0.037364	0.016133	0.990791	TCF8
32360_s_at2281	AF017146	0.047678	0.037364	0.002975	-0.20652	TOP3B
37854_at282	U54996	0.047678	0.037364	0.00691	-0.17359	ZW10
705_at2283	HG4234-HT	0.047678	0.037364	0.003258	-0.13985	
1520_s_at2284	X04500	0.047678	0.058634	0.02228	0.857952	IL1B

Table IV: Differential Gene Expression in MOG-reactive T-cells- MS vs. Healthy

Affymetrix ID no:~~SEQ ID NO:~~	**Identifier**	**Symbol**	**Name**	**Function**	**Fold Change**	**Pvalue t-test**
	Up regulated					
1586_at2285	M35878	IGFBP3	insulin-like growth factor binding protein 3	modulate IGF activity	5.8	0.03
39765_at2286	AB002318	KIAA0320	KIAA0320 protein		2.4	0.05
1953_at2287	AF024710	VEGF	vascular endothelial growth factor	endothelial cell proliferation	2.3	0.02
38829_r_at2288	AA628946	KHSRP	KH-type splicing regulatory protein	mRNA processing	2.2	0.01

635_s_at2289	L42374	PPP2R5B	protein phosphatase 2, regulatory subunit B	protein phosphatase	2.1	0.05
34600_s_at2290	U54644	TUB	tubby (mouse) homolog	may be a transcription factor	1.8	0.01
33293_at2291	AB023167	KIAA0950	lifeguard	Apoptosis	1.8	0.006
37003_at2292	X62654	CD63	CD63 antigen (melanoma 1 antigen)	growth regulation	1.8	0.03
39103_s_at2293	H98552		cDNA DKFZp586I0523		1.8	0.01
35986_at2294	AL050395	MOF	member of MYST acetyl transferases	histone acetyl transferases	1.7	0.03
37490_at2295	L27213	SLC4A3	solute carrier family 4, anion exchange 3	inorganic anion exchanger	1.7	0.01
32246_g_at2296	AF014837	M6A	putative methyltransferase	Transcription factor	1.6	0.05
31788_at2297	AB014537	KIAA0637	KIAA0637 gene product	Apoptosis	1.5	0.003
32192_g_at2298	D13969	ZNF144	zinc finger protein 144 (Mel-18)	DNA-Binding protein	1.5	0.04
34066_at2299	AJ012590	H6PD	hexose-6-phosphate dehydrogenase	Oxidoreductase	1.5	0.04
2060_at2300	M13995	BCL2	B-cell CLL/lymphoma 2	Apoptosis	1.5	0.03
36337_at2301	AI760801		chromosome 19, cosmid R31180		1.5	0.009
40997_at2302	AI660963	MAP3K12	mitogen-activated protein 3 kinase 12	Transferase cytoplasmic	1.5	0.02
	Down regulated					
1184_at2303	D45248	PSME2	proteasome activator subunit 2 (PA28 beta)	Protein degradation	-1.5	0.04
33328_at2304	W28612		ESTs		-1.5	0.02
39105_at2305	Z46389	VASP	vasodilator-stimulated phosphoprotein	Signal transduction	-1.6	0.02
32222_at2306	AA152202	FLJ14639	hypothetical protein FLJ14639		-1.6	0.02
41460_at2307	AF080561	RBM14	RNA binding motif protein 14	RNA binding protein	-1.7	0.03
35322_at2308	D50922	KIAA0132	Kelch-like ECH-associated protein 1	ECH-associated protein 1	-1.7	0.03
37474_at2309	AF025441	OIP5	Opa-interacting protein 5		-1.8	0.04
31853_at2310	AF080227	EED	embryonic ectoderm development	transcriptional repressor	-1.8	0.04
722_at2311	D87957	RQCD1	required for cell differentiation	sex differentiation	-1.9	0.03
40362_at2312	X61498	NFKB2	nuclear factor of kappa light polypeptide Bcells	expression of inflammatory genes	-1.9	0.05
276_at2313	X52425	IL4R	interleukin 4 receptor	receptor signalling protein	-2	0.04
404_at2314	L08069	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	protein folding and transport	-2	0.04
39853_s_at2315	AF071504	STX11	syntaxin 11	protein transport	-2.1	0.03

1104_s_at~~2316~~	M11717	HSPA1A	heat shock 70kD protein 1A	heat shock response	-2.2	0.03
31692_at~~2317~~	M59830	HSPA1B	heat shock 70kD protein 1B	heat shock response	-2.2	0.03
258_at~~2318~~	M16441	TNF	Human tumor necrosis factor	Inflammatory response	-2.3	0.05
1427_g_at~~2319~~	D89077	SLA	Src-like-adapter		-2.4	0.05
37306_at~~2320~~	U77949	CDC6	cell division cycle 6, S. cerevisiae homolog	DNA replication checkpoint	-2.5	0.02
1536_at~~2321~~	D38549	KIAA0068	KIAA0068 protein		-2.5	0.01
1670_at~~2322~~	L23959	TFDP1	transcription factor Dp-1	cycle progression G1 to S-phase	-2.5	0.01
626_s_at~~2323~~	L78833	BRCA1	Breast cancer susceptibility gene		-2.7	0.04
36879_at~~2324~~	M63193	ECGF1	endothelial cell growth factor 1	stimulates angiogenesis	-2.8	0.01
41657_at~~2325~~	AF035625	STK11	serine/threonine kinase 11	Peutz-Jeghers syndrome	-2.9	0.04
36674_at~~2326~~	J04130	SCYA4	small inducible cytokine A4	Cell-to-cell signalling	-2.9	0.05
32613_at~~2327~~	X93086	BLVRA	biliverdin reductase A	biliverdin reductase	-4	0.03

Table V: Differential Gene Expression in Probable MS vs. Healthy

affymetrix ID no:~~SEQ ID NO:~~	Identification	TNOM PValue	Info PValue	t-Test PValue	Log Fold Change	Gene Symbol
218290_at~~2328~~	NM_018049.1	0.000233	0.000233	2.46E-05	0.438337	FLJ10297
203162_s_at~~2329~~	NM_005886.1	0.000233	0.000233	0.000553	0.35972	KATNB1
204224_s_at~~2330~~	NM_000161.1	0.000233	0.000233	0.000297	-0.48848	GCH1
200831_s_at~~2331~~	NM_001539.1	0.000233	0.000233	0.000144	-0.58017	DNAJA1
211699_x_at~~2332~~	AF349571.1	0.004202	0.004202	0.000274	1.78925	HBA1
209116_x_at~~2333~~	M25079.1	0.004202	0.004202	0.000247	1.59503	HBB
217414_x_at~~2334~~	V00489	0.004202	0.004202	0.000268	1.54947	
211745_x_at~~2335~~	BC005931.1	0.004202	0.004202	0.000296	1.48707	HBA2
214414_x_at~~2336~~	T50399	0.004202	0.004202	0.000275	1.43533	HBA2
219259_at~~2337~~	NM_024567.1	0.004202	0.004202	0.002206	1.42146	FLJ21616
209458_x_at~~2338~~	AF105974.1	0.004202	0.004202	0.001086	1.3896	HBA1
204018_x_at~~2339~~	NM_000558.2	0.004202	0.004202	0.000707	1.3348	HBA1
213515_x_at~~2340~~	AI133353	0.004202	0.004202	0.000897	1.29746	HBG2
217232_x_at~~2341~~	AF059180	0.004202	0.004202	0.000309	1.29355	
211696_x_at~~2342~~	AF349114.1	0.004202	0.004202	0.000163	1.27511	HBB
217529_at~~2343~~	BE547674	0.004202	0.004202	0.002947	0.636619	
207641_at~~2344~~	NM_012452.1	0.004202	0.004202	0.000541	0.570818	TNFRSF13B
43544_at~~2345~~	AA314406	0.004202	0.001401	0.002013	0.520631	TRAP95
202926_at~~2346~~	NM_015909.1	0.004202	0.001401	0.000398	0.501733	NAG

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217763_s_at2347	NM_006868.1	0.004202	0.004202	0.002711	0.49862	RAB31
209790_s_at2348	BC000305.1	0.004202	0.004202	0.006921	0.475733	CASP6
32032_at2349	L77566	0.004202	0.001401	0.00033	0.446293	DGSI
205396_at2350	BF971416	0.004202	0.004202	0.002405	0.410742	DKFZP586N0721
202759_s_at2351	BE879367	0.004202	0.004202	0.00056	0.382484	AKAP2
201284_s_at2352	NM_001640.2	0.004202	0.001401	0.004091	0.36631	APEH
205851_at2353	BC001808.1	0.004202	0.004202	0.012997	0.347043	NM23-H6
212194_s_at2354	AL049539	0.004202	0.004202	0.010738	0.2822	KIAA0255
222125_s_at2355	BC000580.1	0.004202	0.001401	0.014166	0.270658	PH-4
203274_at2356	NM_012151.2	0.004202	0.001401	0.000685	0.267664	F8A
217931_at2357	BC004423.1	0.004202	0.004202	0.012194	0.249144	TNRC5
200053_at2358	NM_004890.1	0.004202	0.001401	0.010332	0.134439	SPAG7
40612_at2359	AB029040	0.004202	0.004202	0.010819	-0.14172	KIAA1117
218107_at2360	NM_025160.1	0.004202	0.001401	0.004986	-0.21141	FLJ21016
221873_at2361	AW162015	0.004202	0.004202	0.301224	-0.24766	ZNF143
204249_s_at2362	NM_005574.2	0.004202	0.004202	0.107595	-0.24939	LMO2
200777_s_at2363	NM_014670.1	0.004202	0.004202	0.025534	-0.27225	BZW1
213198_at2364	AL117643.1	0.004202	0.004202	0.046495	-0.27766	
221761_at2365	AA628948	0.004202	0.001401	0.000319	-0.28951	ADSS
211686_s_at2366	AF251062.1	0.004202	0.001401	0.000435	-0.30924	LOC84549
212501_at2367	AL564683	0.004202	0.004202	0.018258	-0.44633	CEBPB
203885_at2368	NM_014999.1	0.004202	0.004202	0.001021	-0.47304	RAB21
219620_x_at2369	NM_017723.1	0.004202	0.004202	0.02759	-0.49548	FLJ20245
204924_at2370	NM_003264.1	0.004202	0.004202	0.002592	-0.49551	TLR2
210275_s_at2371	AF062347.1	0.004202	0.004202	0.00529	-0.51432	ZNF216
203927_at2372	NM_004556.1	0.004202	0.004202	0.001134	-0.53489	NFKBIE
215009_s_at2373	U92014.1	0.004202	0.004202	0.003064	-0.59511	
204435_at2374	NM_014778.1	0.004202	0.004202	0.001106	-0.65156	KIAA0410
207108_s_at2375	NM_015384.1	0.004202	0.004202	0.002943	-0.68193	IDN3
215501_s_at2376	AK022513.1	0.004202	0.004202	0.001326	-0.68416	DUSP10
201110_s_at2377	NM_003246.1	0.004202	0.001401	0.000162	-1.44745	THBS1
201109_s_at2378	AI812030	0.004202	0.001401	7.42E-05	-1.51098	THBS1
204848_x_at2379	NM_000559.1	0.035714	0.035247	0.006202	1.93991	HBG1
204419_x_at2380	NM_000184.1	0.035714	0.04225	0.009164	1.67513	HBG2
212531_at2381	NM_005564.1	0.035714	0.04225	0.010814	1.03322	LCN2
209889_at2382	AF274863.1	0.035714	0.00747	0.007719	0.952868	SEC31B-1
207509_s_at2383	NM_002288.2	0.035714	0.015406	0.010689	0.834313	LAIR2
211430_s_at2384	M87789.1	0.035714	0.04225	0.058518	0.79032	IGHG3
219680_at2385	NM_005764.1	0.035714	0.04225	0.053679	0.789147	DD96
216379_x_at2386	AK000168.1	0.035714	0.04225	0.038176	0.763766	KIAA1919
208161_s_at2387	NM_020037.1	0.035714	0.035247	0.061379	0.746143	ABCC3
216576_x_at2388	AF103529.1	0.035714	0.035247	0.015284	0.736268	
215379_x_at2389	AV698647	0.035714	0.035247	0.017411	0.616137	IGLJ3
214739_at2390	AI357539	0.035714	0.04225	0.00558	0.601843	MGC4126
206468_s_at2391	NM_015935.1	0.035714	0.035247	0.021683	0.593818	CGI-01

37201_at2392	D38535	0.035714	0.04225	0.016025	0.571168	ITIH4
222056_s_at2393	AA723370	0.035714	0.04225	0.039917	0.570325	LOC51011
209322_s_at2394	AF227968.1	0.035714	0.00747	0.005308	0.566516	SH2B
217418_x_at2395	X12530.1	0.035714	0.04225	0.056335	0.559172	MS4A1
214316_x_at2396	AI348935	0.035714	0.035247	0.014129	0.546773	CALR
204139_x_at2397	NM_003422.1	0.035714	0.04225	0.006737	0.536815	ZNF42
205933_at2398	NM_015559.1	0.035714	0.04225	0.028795	0.536316	SETBP1
220058_at2399	NM_013378.1	0.035714	0.035247	0.005191	0.532564	VPREB3
204738_s_at2400	NM_004912.1	0.035714	0.015406	0.003037	0.52082	CCM1
201115_at2401	NM_006230.1	0.035714	0.015406	0.007471	0.517979	POLD2
205267_at2402	NM_006235.1	0.035714	0.035247	0.021726	0.515263	POU2AF1
212955_s_at2403	AL037557	0.035714	0.00747	0.002786	0.511724	POLR2I
204377_s_at2404	NM_014703.1	0.035714	0.00747	0.006709	0.4938	KIAA0800
203871_at2405	NM_015670.1	0.035714	0.035247	0.045708	0.464156	SENP3
213062_at2406	AA643304	0.035714	0.015406	0.004712	0.459694	
203196_at2407	AI948503	0.035714	0.04225	0.017964	0.45625	ABCC4
210356_x_at2408	BC002807.1	0.035714	0.04225	0.100759	0.455683	MS4A1
209586_s_at2409	AF123539.1	0.035714	0.035247	0.028286	0.454603	HTCD37
212813_at2410	AA149644	0.035714	0.00747	0.02413	0.450082	JAM3
210542_s_at2411	BC000585.1	0.035714	0.04225	0.033113	0.44368	SLC21A11
210036_s_at2412	AB044806.1	0.035714	0.04225	0.007766	0.433985	KCNH2
215299_x_at2413	U37025	0.035714	0.035247	0.046971	0.427213	SULT1A1
218440_at2414	NM_020166.2	0.035714	0.035247	0.006318	0.423798	MCCC1
206056_s_at2415	NM_002876.1	0.035714	0.035247	0.026644	0.414867	RAD51C
206132_at2416	NM_002387.1	0.035714	0.035247	0.01092	0.409481	MCC
206761_at2417	NM_005816.1	0.035714	0.04225	0.103051	0.407348	TACTILE
213484_at2418	H95263	0.035714	0.035247	0.069113	0.406766	
200957_s_at2419	NM_003146.1	0.035714	0.035247	0.003146	0.405309	SSRP1
204857_at2420	NM_003550.1	0.035714	0.035247	0.054105	0.403851	MAD1L1
212932_at2421	AK022494.1	0.035714	0.00747	0.001189	0.397073	RAB3GAP
200932_s_at2422	NM_006400.2	0.035714	0.035247	0.021072	0.396297	DCTN2
202799_at2423	NM_006012.1	0.035714	0.035247	0.015241	0.394779	CLPP
203488_at2424	NM_014921.1	0.035714	0.035247	0.014463	0.394308	LEC2
207758_at2425	NM_025056.1	0.035714	0.00747	0.01912	0.393739	FLJ23185
204442_x_at2426	NM_003573.1	0.035714	0.04225	0.026053	0.393337	LTBP4
205756_s_at2427	NM_000132.2	0.035714	0.035247	0.005292	0.392442	F8
210140_at2428	AF031824.1	0.035714	0.035247	0.190243	0.389129	CST7
206536_at2429	NM_001841.1	0.035714	0.035247	0.07115	0.387067	CNR2
220078_at2430	NM_018391.1	0.035714	0.035247	0.138584	0.386982	FLJ23277
215283_at2431	U79248.1	0.035714	0.00747	0.007475	0.386419	
221196_x_at2432	NM_024332.1	0.035714	0.04225	0.039154	0.386198	C6.1A
221969_at2433	BF510692	0.035714	0.04225	0.046782	0.385324	PAX5
49679_s_at2434	AA243774	0.035714	0.035247	0.050456	0.381631	MMP24
206853_s_at2435	AL121964	0.035714	0.035247	0.107681	0.373759	MAP3K7
210530_x_at2436	L25275.1	0.035714	0.035247	0.020684	0.372971	SULT1A3
212314_at2437	AB018289.1	0.035714	0.035247	0.002286	0.37263	KIAA0746

203709_at2438	NM_000294.1	0.035714	0.035247	0.011432	0.367693	PHKG2
210386_s_at2439	BC001906.1	0.035714	0.035247	0.107947	0.366899	MTX1
208488_s_at2440	NM_000651.1	0.035714	0.04225	0.047953	0.365471	CR1
202564_x_at2441	NM_001667.1	0.035714	0.00747	0.009661	0.362105	ARL2
213051_at2442	AI133727	0.035714	0.00747	0.018354	0.358884	ZAP
209177_at2443	BC002873.1	0.035714	0.035247	0.048711	0.358052	DKFZP564J0123
203677_s_at2444	NM_004178.2	0.035714	0.035247	0.007313	0.356459	TARBP2
201138_s_at2445	BG532929	0.035714	0.035247	0.037215	0.356254	SSB
205541_s_at2446	NM_018094.1	0.035714	0.035247	0.014302	0.351314	GSPT2
40255_at2447	AC004531	0.035714	0.00747	0.01714	0.350445	DDX28
217837_s_at2448	NM_001981.1	0.035714	0.035247	0.010776	0.347051	EPS15
212960_at2449	AB020689.1	0.035714	0.035247	0.024594	0.346253	KIAA0882
203615_x_at2450	NM_001055.1	0.035714	0.035247	0.056416	0.344937	SULT1A1
218431_at2451	NM_022067.1	0.035714	0.035247	0.001332	0.337713	FLJ12707
203309_s_at2452	NM_000195.1	0.035714	0.00747	0.014156	0.3312	HPS1
204617_s_at2453	NM_022914.1	0.035714	0.00747	0.167735	0.331082	24432
204394_at2454	NM_003627.1	0.035714	0.035247	0.062759	0.330371	POV1
218581_at2455	NM_022060.1	0.035714	0.035247	0.010717	0.328122	FLJ12816
213581_at2456	BF446180	0.035714	0.035247	0.02537	0.326347	PDCD2
211385_x_at2457	U28169.1	0.035714	0.035247	0.0891	0.326218	SULT1A2
209019_s_at2458	AF316873.1	0.035714	0.035247	0.022727	0.3257	PINK1
219067_s_at2459	NM_017615.1	0.035714	0.035247	0.087717	0.325056	FLJ20003
201871_s_at2460	NM_015853.1	0.035714	0.035247	0.021537	0.321089	LOC51035
219192_at2461	NM_018449.1	0.035714	0.035247	0.01461	0.318475	UBAP2
204978_at2462	NM_007056.1	0.035714	0.035247	0.013827	0.318086	SWAP2
215691_x_at2463	AV702994	0.035714	0.035247	0.010766	0.316138	LOC51668
215090_x_at2464	AK021884.1	0.035714	0.04225	0.016862	0.315879	NPEPPS
208709_s_at2465	U64898.1	0.035714	0.035247	0.012705	0.309446	NRD1
44617_at2466	AI431902	0.035714	0.035247	0.026163	0.307321	FLJ13491
202139_at2467	NM_003689.1	0.035714	0.04225	0.03366	0.306281	AKR7A2
203289_s_at2468	BE791629	0.035714	0.00747	0.039522	0.304821	CGTHBA
204000_at2469	NM_016194.1	0.035714	0.035247	0.060249	0.303474	GNB5
202080_s_at2470	NM_014965.1	0.035714	0.035247	0.013547	0.298042	KIAA1042
202682_s_at2471	NM_003363.1	0.035714	0.035247	0.018393	0.295239	USP4
33304_at2472	U88964	0.035714	0.035247	0.019349	0.294427	ISG20
209729_at2473	BC001782.1	0.035714	0.035247	0.059026	0.293156	GAS2L1
209158_s_at2474	BC004361.1	0.035714	0.04225	0.084538	0.292509	PSCD2
217980_s_at2475	NM_017840.1	0.035714	0.035247	0.003929	0.290472	MRPL16
201230_s_at2476	NM_006321.1	0.035714	0.015406	0.006688	0.288723	ARIH2
64486_at2477	AI341234	0.035714	0.035247	0.007356	0.284699	CORO1B
212486_s_at2478	N20923	0.035714	0.035247	0.020271	0.280552	FYN
211630_s_at2479	L42531.1	0.035714	0.035247	0.008554	0.280023	
214749_s_at2480	AK000818.1	0.035714	0.035247	0.02226	0.277695	FLJ20811
203685_at2481	NM_000633.1	0.035714	0.035247	0.044639	0.276897	BCL2
213607_x_at2482	BE551347	0.035714	0.035247	0.209003	0.276406	FLJ13052
202808_at2483	AK000161.1	0.035714	0.04225	0.016752	0.276103	FLJ20154

212735_at2484	AI798908	0.035714	0.04225	0.015969	0.274921	KIAA0226
219767_s_at2485	NM_005111.1	0.035714	0.035247	0.01405	0.273732	CRYZL1
201346_at2486	NM_024551.1	0.035714	0.035247	0.00372	0.272684	FLJ21432
221708_s_at2487	BC006214.1	0.035714	0.00747	0.006244	0.268704	IRO039700
203492_x_at2488	AI123527	0.035714	0.04225	0.105392	0.268349	KIAA0092
204313_s_at2489	NM_004379.1	0.035714	0.035247	0.047229	0.267796	CREB1
213061_s_at2490	AA643304	0.035714	0.035247	0.039678	0.258201	
204744_s_at2491	NM_013417.1	0.035714	0.035247	0.047087	0.257738	IARS
212946_at2492	AK025432.1	0.035714	0.035247	0.051871	0.257456	KIAA0564
40829_at2493	AB028960	0.035714	0.04225	0.040942	0.254827	KIAA1037
204608_at2494	NM_000048.1	0.035714	0.04225	0.038931	0.254447	ASL
200830_at2495	NM_002808.1	0.035714	0.035247	0.023966	0.250129	PSMD2
207122_x_at2496	NM_001054.1	0.035714	0.035247	0.062598	0.248696	SULT1A2
206219_s_at2497	NM_005428.2	0.035714	0.035247	0.007185	0.248439	VAV1
217925_s_at2498	NM_022758.1	0.035714	0.04225	0.011489	0.246401	FLJ22195
209075_s_at2499	AY009128.1	0.035714	0.035247	0.084938	0.246257	NIFU
214756_x_at2500	AB017004.1	0.035714	0.035247	0.079567	0.244954	PMS2L8
202520_s_at2501	NM_000249.1	0.035714	0.04225	0.021274	0.243441	MLH1
211609_x_at2502	U51007.1	0.035714	0.035247	0.042753	0.242223	
210312_s_at2503	BC002640.1	0.035714	0.035247	0.074751	0.240603	
200861_at2504	NM_016284.1	0.035714	0.00747	0.001929	0.240076	KIAA1007
201029_s_at2505	NM_002414.1	0.035714	0.035247	0.063998	0.239013	MIC2
210620_s_at2506	BC000212.1	0.035714	0.035247	0.021052	0.237577	GTF3C2
204977_at2507	NM_004398.2	0.035714	0.035247	0.040656	0.235252	DDX10
218791_s_at2508	NM_024713.1	0.035714	0.035247	0.048887	0.234927	FLJ22557
200832_s_at2509	NM_002810.1	0.035714	0.035247	0.038558	0.234593	PSMD4
219801_at2510	NM_030580.1	0.035714	0.035247	0.031263	0.233466	MGC10520
212216_at2511	AB007896.1	0.035714	0.035247	0.211816	0.231563	KIAA0436
205192_at2512	NM_003954.1	0.035714	0.04225	0.051916	0.230862	MAP3K14
205661_s_at2513	NM_025207.1	0.035714	0.035247	0.020823	0.230015	PP591
219863_at2514	NM_016323.1	0.035714	0.035247	0.051393	0.228764	LOC51191
218969_at2515	NM_016069.1	0.035714	0.04225	0.132766	0.223618	Magmas
218407_x_at2516	NM_013349.1	0.035714	0.035247	0.028748	0.223073	SPUF
201892_s_at2517	NM_000884.1	0.035714	0.035247	0.064347	0.222421	IMPDH2
222264_at2518	BG167570	0.035714	0.04225	0.108243	0.219652	DKFZp762N1910
201740_at2519	NM_004551.1	0.035714	0.00747	0.06025	0.217427	NDUFS3
200742_s_at2520	BG231932	0.035714	0.04225	0.079649	0.210447	CLN2
219034_at2521	NM_017851.1	0.035714	0.035247	0.036308	0.209956	FLJ20509
201999_s_at2522	NM_006519.1	0.035714	0.035247	0.032991	0.202387	TCTEL1
209746_s_at2523	AF032900.1	0.035714	0.035247	0.174549	0.200739	COQ7
200920_s_at2524	AL535380	0.035714	0.035247	0.265205	0.198073	BTG1
203704_s_at2525	AW118862	0.035714	0.035247	0.02173	0.193753	RREB1
202054_s_at2526	NM_000382.1	0.035714	0.035247	0.27948	0.193509	ALDH3A2
219394_at2527	NM_024419.1	0.035714	0.035247	0.164883	0.190623	PGS1
200054_at2528	NM_003904.1	0.035714	0.035247	0.245676	0.190422	ZNF259
209971_x_at2529	AI928526	0.035714	0.00747	0.036861	0.185624	JTV1

220150_s_at2530	NM_024581.1	0.035714	0.035247	0.230867	0.185323	FLJ13942
208749_x_at2531	AF085357.1	0.035714	0.035247	0.110175	0.184965	FLOT1
201350_at2532	NM_004475.1	0.035714	0.035247	0.072642	0.180483	FLOT2
221699_s_at2533	AF334103.1	0.035714	0.00747	0.009664	0.17511	GU2
218592_s_at2534	NM_017829.1	0.035714	0.035247	0.110207	0.174515	CECR5
202041_s_at2535	NM_004214.3	0.035714	0.04225	0.016835	0.157902	FIBP
219069_at2536	NM_017704.1	0.035714	0.04225	0.16159	0.157672	FLJ20189
207614_s_at2537	NM_003592.1	0.035714	0.035247	0.038652	0.146241	CUL1
201060_x_at2538	AI537887	0.035714	0.035247	0.467375	0.139355	EPB72
218159_at2539	NM_023935.1	0.035714	0.035247	0.049119	0.125305	C20orf116
201528_at2540	BG398414	0.035714	0.035247	0.286856	0.123085	RPA1
202263_at2541	NM_016243.1	0.035714	0.035247	0.279995	0.121894	LOC51706
218287_s_at2542	NM_012199.1	0.035714	0.035247	0.093241	0.118547	EIF2C1
212508_at2543	AK024029.1	0.035714	0.04225	0.450393	0.11646	MAP-1
207571_x_at2544	NM_004848.1	0.035714	0.035247	0.486492	0.113516	ICB-1
212322_at2545	AF144638.1	0.035714	0.035247	0.255571	0.10089	SGPL1
210667_s_at2546	D86062.1	0.035714	0.035247	0.532398	0.084417	C21orf33
204563_at2547	NM_000655.2	0.035714	0.035247	0.535745	0.081167	SELL
219434_at2548	NM_018643.1	0.035714	0.035247	0.870775	0.057399	TREM1
219243_at2549	NM_018326.1	0.035714	0.035247	0.929375	0.035048	HIMAP4
204027_s_at2550	NM_005371.2	0.035714	0.035247	0.876737	0.025127	METTL1
201281_at2551	NM_007002.1	0.035714	0.035247	0.911541	0.010422	ADRM1
207629_s_at2552	NM_004723.1	0.035714	0.035247	0.975685	-0.00562	ARHGEF2
35265_at2553	U31501	0.035714	0.035247	0.724549	-0.0658	FXR2
205425_at2554	NM_005338.3	0.035714	0.04225	0.126911	-0.0661	HIP1
210780_at2555	AB006589.1	0.035714	0.035247	0.00542	-0.10655	ESR2
212569_at2556	AA868754	0.035714	0.035247	0.304519	-0.10746	KIAA0650
215671_at2557	AU144792	0.035714	0.035247	0.008623	-0.11362	
214629_x_at2558	AF320999.1	0.035714	0.035247	0.289096	-0.11449	RTN4
204859_s_at2559	NM_013229.1	0.035714	0.035247	0.529181	-0.13735	APAF1
220023_at2560	NM_018690.1	0.035714	0.04225	0.261146	-0.14482	APOB48R
213012_at2561	D42055.1	0.035714	0.04225	0.007978	-0.14841	NEDD4
212696_s_at2562	BF968633	0.035714	0.035247	0.135003	-0.14873	RNF4
209022_at2563	AK026678.1	0.035714	0.035247	0.00833	-0.15056	STAG2
201817_at2564	NM_014671.1	0.035714	0.035247	0.392979	-0.15386	KIAA0010
208113_x_at2565	NM_030979.1	0.035714	0.035247	0.087494	-0.15652	PABPC3
215022_x_at2566	BG429214	0.035714	0.035247	0.273519	-0.15766	
220668_s_at2567	NM_006892.1	0.035714	0.035247	0.001922	-0.15828	DNMT3B
201174_s_at2568	NM_018975.1	0.035714	0.035247	0.042202	-0.16723	RAP1
200994_at2569	AL137335.1	0.035714	0.035247	0.306422	-0.17292	RANBP7
202797_at2570	NM_014016.1	0.035714	0.035247	0.398036	-0.17365	SACM1L
203765_at2571	NM_012198.1	0.035714	0.035247	0.391555	-0.17556	GCA
218047_at2572	NM_024586.1	0.035714	0.04225	0.011965	-0.19298	OSBPL9
201964_at2573	N64643	0.035714	0.035247	0.16498	-0.19313	KIAA0625
206461_x_at2574	NM_005951.1	0.035714	0.035247	0.156965	-0.1942	MT1H
202055_at2575	NM_002264.1	0.035714	0.035247	0.138195	-0.1949	

217856_at~~2576~~	AF182415.1	0.035714	0.04225	0.325959	-0.19495	RBM8A
214225_at~~2577~~	BE674061	0.035714	0.035247	0.015036	-0.20133	PIN4
203298_s_at~~2578~~	NM_004973.2	0.035714	0.00747	0.103071	-0.20162	JMJ
211584_s_at~~2579~~	U58852.1	0.035714	0.035247	0.510508	-0.20606	NPAT
205270_s_at~~2580~~	NM_005565.2	0.035714	0.035247	0.037541	-0.2105	LCP2
203364_at~~2581~~	NM_004941.1	0.035714	0.035247	0.229189	-0.21215	DDX8
209880_s_at~~2582~~	U02297.1	0.035714	0.035247	0.252672	-0.21782	SELPLG
201873_s_at~~2583~~	NM_002940.1	0.035714	0.035247	0.112373	-0.22731	ABCE1
208677_s_at~~2584~~	AL550657	0.035714	0.035247	0.069403	-0.23303	BSG
222283_at~~2585~~	BG387770	0.035714	0.035247	0.032984	-0.2362	MGC32104
212714_at~~2586~~	AL050205.1	0.035714	0.04225	0.352078	-0.23748	LOC113251
218883_at~~2587~~	NM_016653.1	0.035714	0.035247	0.003387	-0.23765	ZAK
214201_x_at~~2588~~	AA742237	0.035714	0.035247	0.120935	-0.23853	BAT2
218659_at~~2589~~	NM_021183.1	0.035714	0.035247	0.069121	-0.24239	LOC57826
212306_at~~2590~~	AB014527.1	0.035714	0.035247	0.005636	-0.24315	CLASP2
213379_at~~2591~~	AF091086.1	0.035714	0.035247	0.124853	-0.24621	CL640
203761_at~~2592~~	NM_006748.1	0.035714	0.04225	0.141473	-0.24728	SLA
217945_at~~2593~~	NM_025238.1	0.035714	0.035247	0.046507	-0.24841	BTBD1
219017_at~~2594~~	NM_018638.2	0.035714	0.035247	0.074405	-0.24942	EKI1
208021_s_at~~2595~~	NM_002913.1	0.035714	0.04225	0.092197	-0.24967	
202990_at~~2596~~	NM_002863.1	0.035714	0.035247	0.034567	-0.25494	PYGL
209431_at~~2597~~	AF226044.1	0.035714	0.035247	0.023966	-0.25679	SNRK
218603_at~~2598~~	NM_016217.1	0.035714	0.035247	0.01673	-0.25733	LOC51696
209535_s_at~~2599~~	AF084943.1	0.035714	0.035247	0.024841	-0.26011	MINPP1
213044_at~~2600~~	N22548	0.035714	0.04225	0.03686	-0.26164	ROCK1
209643_s_at~~2601~~	AF033850.1	0.035714	0.035247	0.110532	-0.26338	PLD2
200971_s_at~~2602~~	NM_014445.1	0.035714	0.00747	0.007058	-0.26858	SERP1
205115_s_at~~2603~~	NM_016196.1	0.035714	0.035247	0.014278	-0.27109	KIAA0682
206715_at~~2604~~	NM_012252.1	0.035714	0.035247	0.020625	-0.27124	TFEC
202877_s_at~~2605~~	W72082	0.035714	0.035247	0.180599	-0.27284	C1QR1
217863_at~~2606~~	NM_016166.1	0.035714	0.035247	0.071782	-0.27429	PIAS1
219628_at~~2607~~	NM_022470.1	0.035714	0.035247	0.072884	-0.27655	WIG1
208092_s_at~~2608~~	NM_030797.1	0.035714	0.035247	0.039197	-0.27728	DKFZP566A1524
203275_at~~2609~~	NM_002199.2	0.035714	0.035247	0.250656	-0.27789	IRF2
208896_at~~2610~~	BC003360.1	0.035714	0.035247	0.02171	-0.27851	DDX18
218092_s_at~~2611~~	NM_004504.2	0.035714	0.035247	0.020834	-0.27873	HRB
202878_s_at~~2612~~	NM_012072.2	0.035714	0.035247	0.118494	-0.27892	C1QR1
202184_s_at~~2613~~	NM_018230.1	0.035714	0.035247	0.071301	-0.28019	NUP133
201859_at~~2614~~	NM_002727.1	0.035714	0.04225	0.038559	-0.28438	PRG1
201238_s_at~~2615~~	BC005338.1	0.035714	0.035247	0.114062	-0.28524	CAPZA2
203984_s_at~~2616~~	U60521.1	0.035714	0.04225	0.066643	-0.29174	CASP9
206025_s_at~~2617~~	AW188198	0.035714	0.035247	0.005126	-0.29178	TNFAIP6
213129_s_at~~2618~~	BE908931	0.035714	0.035247	0.017009	-0.29572	
215823_x_at~~2619~~	U64661	0.035714	0.04225	0.030982	-0.29704	
217346_at~~2620~~	AL021395	0.035714	0.04225	0.02084	-0.29857	
202272_s_at~~2621~~	NM_015176.1	0.035714	0.035247	0.059688	-0.299	KIAA0483

201707_at2622	NM_002857.1	0.035714	0.04225	0.04761	-0.29944	PXF
209124_at2623	U70451.1	0.035714	0.035247	0.003458	-0.30169	MYD88
219885_at2624	NM_018042.1	0.035714	0.035247	0.020209	-0.30409	FLJ10260
212195_at2625	AL049265.1	0.035714	0.04225	0.136618	-0.30472	
207291_at2626	NM_024081.1	0.035714	0.035247	0.020267	-0.30513	TMG4
209602_s_at2627	AI796169	0.035714	0.035247	0.023959	-0.31104	GATA3
213291_s_at2628	AA160522	0.035714	0.035247	0.056044	-0.31114	UBE3A
210281_s_at2629	AL136621.1	0.035714	0.04225	0.06859	-0.31538	ZNF198
202236_s_at2630	NM_003051.1	0.035714	0.035247	0.028776	-0.3171	SLC16A1
212286_at2631	AW572909	0.035714	0.035247	0.027025	-0.31713	KIAA0874
218381_s_at2632	NM_017782.1	0.035714	0.04225	0.017104	-0.32078	FLJ20360
212959_s_at2633	AK001821.1	0.035714	0.04225	0.013182	-0.32145	MGC4170
214875_x_at2634	AW001847	0.035714	0.035247	0.204195	-0.32259	APLP2
203730_s_at2635	BF196931	0.035714	0.04225	0.003706	-0.3226	ZFP95
206308_at2636	AJ223333.1	0.035714	0.035247	0.023593	-0.32279	DNMT2
204971_at2637	NM_005213.1	0.035714	0.04225	0.216305	-0.32285	CSTA
212262_at2638	AF142419.1	0.035714	0.04225	0.013772	-0.33425	QKI
219099_at2639	NM_020375.1	0.035714	0.035247	0.07666	-0.33473	C12orf5
217971_at2640	NM_021970.1	0.035714	0.04225	0.054987	-0.33505	MAP2K1IP1
215006_at2641	AK023816.1	0.035714	0.035247	0.136952	-0.34214	
218878_s_at2642	NM_012238.3	0.035714	0.00747	0.018308	-0.3438	SIRT1
201362_at2643	AF205218.1	0.035714	0.035247	0.033088	-0.34674	NS1-BP
201097_s_at2644	NM_001660.2	0.035714	0.035247	0.020387	-0.35015	ARF4
204493_at2645	NM_001196.1	0.035714	0.015406	0.020544	-0.35511	BID
203455_s_at2646	NM_002970.1	0.035714	0.035247	0.064201	-0.35676	SAT
217403_s_at2647	AC074331	0.035714	0.035247	0.01515	-0.35767	
201573_s_at2648	M75715.1	0.035714	0.035247	0.010802	-0.3577	ETF1
218926_at2649	NM_018657.2	0.035714	0.04225	0.021807	-0.3681	MYNN
202205_at2650	NM_003370.1	0.035714	0.035247	0.056143	-0.37617	VASP
202934_at2651	AI761561	0.035714	0.035247	0.084393	-0.37861	HK2
202925_s_at2652	NM_002657.2	0.035714	0.035247	0.043402	-0.39004	PLAGL2
203503_s_at2653	NM_004565.1	0.035714	0.035247	0.086212	-0.39025	PEX14
212209_at2654	AK023837.1	0.035714	0.04225	0.083366	-0.39056	KIAA1025
202194_at2655	AL117354	0.035714	0.00747	0.011916	-0.39754	LOC50999
201210_at2656	NM_001356.2	0.035714	0.035247	0.029134	-0.41337	DDX3
218041_x_at2657	NM_018573.1	0.035714	0.015406	0.00529	-0.41757	PRO1068
221423_s_at2658	NM_030799.1	0.035714	0.035247	0.075235	-0.42088	SMAP-5
213649_at2659	AA524053	0.035714	0.04225	0.031361	-0.42442	
207121_s_at2660	NM_002748.1	0.035714	0.035247	0.023266	-0.42563	MAPK6
202270_at2661	NM_002053.1	0.035714	0.035247	0.053201	-0.43747	GBP1
212838_at2662	AB023227.1	0.035714	0.04225	0.003343	-0.43985	KIAA1010
202814_s_at2663	AW193511	0.035714	0.035247	0.012709	-0.44652	HIS1
203432_at2664	AW272611	0.035714	0.04225	0.024277	-0.44899	TMPO
212644_s_at2665	AI671747	0.035714	0.00747	0.02288	-0.45263	MISS
209362_at2666	AI688580	0.035714	0.035247	0.035918	-0.45484	SURB7
207535_s_at2667	NM_002502.1	0.035714	0.035247	0.107712	-0.45745	NFKB2

203921_at2668	NM_004267.1	0.035714	0.04225	0.030352	-0.47177	CHST2
216841_s_at2669	X15132.1	0.035714	0.035247	0.041452	-0.47259	SOD2
219308_s_at2670	NM_012093.1	0.035714	0.035247	0.011606	-0.47474	AK5
212623_at2671	D26067.1	0.035714	0.035247	0.003438	-0.47644	KIAA0033
202076_at2672	NM_001166.2	0.035714	0.04225	0.015252	-0.48334	BIRC2
218611_at2673	NM_016545.1	0.035714	0.035247	0.029826	-0.48723	IER5
201963_at2674	NM_021122.2	0.035714	0.035247	0.070882	-0.49855	FACL2
220369_at2675	NM_017936.1	0.035714	0.035247	0.008293	-0.5016	FLJ20707
201925_s_at2676	NM_000574.1	0.035714	0.035247	0.022743	-0.50532	DAF
212749_s_at2677	AL050144.1	0.035714	0.015406	0.000822	-0.52839	ZNF363
202581_at2678	NM_005346.2	0.035714	0.035247	0.10824	-0.5359	HSPA1B
218689_at2679	NM_022725.1	0.035714	0.035247	0.023814	-0.53779	FANCF
200962_at2680	AI348010	0.035714	0.035247	0.226116	-0.54348	
201799_s_at2681	AI927993	0.035714	0.035247	0.054067	-0.54478	OSBP
213281_at2682	BE327172	0.035714	0.035247	0.091317	-0.54925	JUN
213021_at2683	AI741876	0.035714	0.00747	0.025182	-0.57505	
201416_at2684	NM_003107.1	0.035714	0.035247	0.078087	-0.59709	SOX4
216300_x_at2685	BE383139	0.035714	0.035247	0.00951	-0.60058	RARA
219714_s_at2686	NM_018398.1	0.035714	0.035247	0.016221	-0.603	CACNA2D3
202638_s_at2687	NM_000201.1	0.035714	0.035247	0.036915	-0.62554	ICAM1
201473_at2688	NM_002229.1	0.035714	0.035247	0.129802	-0.64436	JUNB
200798_x_at2689	NM_021960.1	0.035714	0.04225	0.024176	-0.66914	MCL1
205308_at2690	NM_016010.1	0.035714	0.00747	0.015684	-0.68307	LOC51101
201041_s_at2691	NM_004417.2	0.035714	0.035247	0.043377	-0.68458	DUSP1
202241_at2692	NM_025195.1	0.035714	0.035247	0.055882	-0.68638	C8FW
204794_at2693	NM_004418.2	0.035714	0.035247	0.306591	-0.68934	DUSP2
208961_s_at2694	AB017493.1	0.035714	0.015406	0.010224	-0.6982	COPEB
209545_s_at2695	AF064824.1	0.035714	0.035247	0.010071	-0.70109	RIPK2
203751_x_at2696	NM_005354.2	0.035714	0.035247	0.04394	-0.70667	JUND
206245_s_at2697	NM_006469.1	0.035714	0.035247	0.006453	-0.71493	NS1-BP
202644_s_at2698	NM_006290.1	0.035714	0.035247	0.155375	-0.73437	TNFAIP3
214326_x_at2699	AI339541	0.035714	0.035247	0.039838	-0.76402	JUND
209304_x_at2700	AF087853.1	0.035714	0.035247	0.076647	-0.77217	GADD45B
216336_x_at2701	AL031602	0.035714	0.035247	0.015158	-0.78504	
221477_s_at2702	BF575213	0.035714	0.035247	0.007144	-0.78651	
201670_s_at2703	M68956.1	0.035714	0.00747	0.001933	-0.79718	MARCKS
202081_at2704	NM_004907.1	0.035714	0.035247	0.006503	-0.81053	ETR101
212659_s_at2705	AW083357	0.035714	0.035247	0.009893	-0.81405	IL1RN
206765_at2706	AF153820.1	0.035714	0.035247	0.004403	-0.82757	KCNJ2
202637_s_at2707	AI608725	0.035714	0.035247	0.010119	-0.83319	ICAM1
204897_at2708	NM_000958.1	0.035714	0.015406	0.003112	-0.86354	PTGER4
214211_at2709	AA083483	0.035714	0.035247	0.012228	-0.88452	FTH1
203471_s_at2710	NM_002664.1	0.035714	0.00747	0.000855	-0.88664	PLEK
213038_at2711	AL031602	0.035714	0.015406	0.00038	-0.88673	
36564_at2712	W27419	0.035714	0.015406	0.000361	-0.95575	
206157_at2713	NM_002852.1	0.035714	0.035247	0.001716	-0.97365	PTX3

201694_s_at~~2714~~	NM_001964.1	0.035714	0.035247	0.068287	-0.99045	EGR1
209305_s_at~~2715~~	AF078077.1	0.035714	0.035247	0.017058	-1.003	GADD45B
213524_s_at~~2716~~	NM_015714.1	0.035714	0.035247	0.210858	-1.05996	G0S2
209189_at~~2717~~	BC004490.1	0.035714	0.035247	0.068201	-1.06388	FOS
202643_s_at~~2718~~	AI738896	0.035714	0.035247	0.071526	-1.09453	TNFAIP3
222326_at~~2719~~	AW973834	0.035714	0.035247	0.030817	-1.09468	
207075_at~~2720~~	NM_004895.1	0.035714	0.035247	0.004992	-1.10724	CIAS1
210845_s_at~~2721~~	U08839.1	0.035714	0.035247	0.030968	-1.1245	PLAUR
201489_at~~2722~~	BC005020.1	0.035714	0.035247	0.022893	-1.13801	PPIF
201739_at~~2723~~	NM_005627.1	0.035714	0.035247	0.010834	-1.16132	SGK
207574_s_at~~2724~~	NM_015675.1	0.035714	0.035247	0.022251	-1.16822	GADD45B
203470_s_at~~2725~~	AI433595	0.035714	0.015406	0.002395	-1.17663	PLEK
202340_x_at~~2726~~	NM_002135.1	0.035714	0.035247	0.009942	-1.19934	NR4A1
201531_at~~2727~~	NM_003407.1	0.035714	0.035247	0.0028	-1.30448	ZFP36
204440_at~~2728~~	NM_004233.1	0.035714	0.035247	0.045128	-1.33091	CD83
205767_at~~2729~~	NM_001432.1	0.035714	0.035247	0.001942	-1.33633	EREG
201466_s_at~~2730~~	NM_002228.2	0.035714	0.035247	0.007227	-1.34352	JUN
205681_at~~2731~~	NM_004049.1	0.035714	0.035247	0.004927	-1.41895	BCL2A1
37028_at~~2732~~	U83981	0.035714	0.035247	0.005806	-1.46885	PPP1R15A
205220_at~~2733~~	NM_006018.1	0.035714	0.035247	0.002094	-1.50671	HM74
201464_x_at~~2734~~	BG491844	0.035714	0.035247	0.011957	-1.61438	JUN
201465_s_at~~2735~~	BC002646.1	0.035714	0.035247	0.002438	-1.64136	JUN
204748_at~~2736~~	NM_000963.1	0.035714	0.035247	0.025772	-1.65759	PTGS2
211924_s_at~~2737~~	AY029180.1	0.035714	0.035247	0.011082	-1.69399	PLAUR
202014_at~~2738~~	NM_014330.2	0.035714	0.035247	0.003245	-1.74665	PPP1R15A
201631_s_at~~2739~~	NM_003897.1	0.035714	0.035247	0.002981	-1.89968	IER3
209774_x_at~~2740~~	M57731.1	0.035714	0.035247	0.001811	-1.9703	CXCL2
202859_x_at~~2741~~	NM_000584.1	0.035714	0.035247	0.030747	-2.54298	IL8
205067_at~~2742~~	NM_000576.1	0.035714	0.035247	0.000992	-2.66025	IL1B
39402_at~~2743~~	M15330	0.035714	0.035247	0.001505	-2.71142	IL1B

It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable subcombination.

Although the invention has been described in conjunction with specific embodiments thereof, it is evident that many alternatives, modifications and

variations will be apparent to those skilled in the art. Accordingly, it is intended to embrace all such alternatives, modifications and variations that fall within the spirit and broad scope of the appended claims. All publications, patents, patent applications and sequences identifies by a GenBank accession number mentioned in this specification are herein incorporated in their entirety by reference into the specification, to the same extent as if each individual publication, patent, patent application or sequence was specifically and individually indicated to be incorporated herein by reference. In addition, citation or identification of any reference in this application shall not be construed as an admission that such reference is available as prior art to the present invention.

ABSTRACT

Markers of multiple sclerosis and methods and kits utilizing same for diagnosing multiple sclerosis in an individual are provided.